GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Run
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Maximum Match 100%
Listing first 45 summaries
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 pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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protein search, using sw model
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/cgm2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/FCTUS_COMB.pep:*
/cgm2_6/ptcdata/2/iaa/backfiles1.pep:*
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US-10-182-263-3
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137.669 Million cell updates/sec
  Sequence 4,
Patent No. 52
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Sequence 2,
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Sequence 5, Appli
Sequence 35, Appli
Sequence 3, Appli
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Sequence 5, Appli
Sequence 20, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 25, Appli
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              APPLICANT: Geriltz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
COMMUNER: DATE: 2000-03-14
                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                         Sequence 6, Application US/10182263 Patent No. 6630138
                                                                                                                                                                                                                                                                                                    Matches
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      version 3.1
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sequence 3, Appri	equence	equence 2, App1	equence 2, Appl	equence 2, Appl	equence 2, Appr	equence 2, Appr	e 23, Ap	equence i,	equence I, Appr	equence 2,	equence 2, Appr	equence 8, Appr	equence 5,	0. 02/01/	sequence a, Appr	Celic No. 54	ent No. 527017

ALIGNMENTS

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PATENT NO. 6017882

PATENT NO. 6017882

APPLICANT: Nelsestuen, GATY
APPLICANT: Nelsestuen, GATY
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPETIDES
FILL, REFERENCE: 09521/002001

FULL, REFERENCE: 09521/002001

CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PATENDER HOMO SAPIENS
PERATURE:
PERATURE
                                                                                                                       ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                             90.9%; So ilarity 100.0%; I Conservative 0;
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GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gorinell, Brian W
ITILE OF INVENTION: PROTEIN C DERIVATIVES
FILE RETERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-12
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 12
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US-10-182-263-3
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                                                            ; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-3
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CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35
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Patent No. 6017882
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Patent No. 663013
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Best Local
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Query Match
Best Local Similarity
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TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD_RES
LOCATION: (0)...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
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Local Similarity 79.5%;
les 35; Conservative
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88.3%;
77.3%;
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Pred. No. 6.9e-23;
1; Mismatches 0
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Score 174; DB 4; Length 419; Pred. No. 2e-21;
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Sequence 5, Application US/10182263

Patent No. 6630138

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E

APPLICANT: Grinnell, Brian W

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-1361

CURRENT APPLICATION NUMBER: US/10/182,263

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: 60/181948

PRIOR FILING DATE: 2002-03-14

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5
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US-10-182-263-5
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US-10-182-263-4
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Patent No. 6630138
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
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Best Local (
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR APPLICATION NUMBER: 60/189199
PRIOR APPLICATION NUMBER: 60/189199
PRIOR APPLICATION DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                      LENGTH: 4:
TYPE: PRT
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                                                                                                           Similarity
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  ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.3%; Score 174; DB 4
77.3%; Pred. No. 2e-21;
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                                                                                   Score 174; DB 4; Length 419; Pred. No. 2e-21; 0; Mismatches 10; Indels
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RESULT 9
US-08-955-636-19
; Sequence 19, Applicat.
; Patent No. 6017882
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                             ; NAME/KRY: MOD_RES; LOCATION: (0) ... (0) ... OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid US-08-955-636-21
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US-08-955-636-20
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APPLICANT: Nelsestu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 21, Application Patent No. 6017882 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Appli
Patent No. 6017882
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE: NAME/KEY: MOD_RES LOCATION: (0)...(0) OTHER INFORMATION: Xaa=
                                                                                                                                                                                                                                                                      Matches
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TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILLING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT TITLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 09531/002001
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LENGTH: 44
TYPE: PRT
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APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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97.7%;
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                                                                                                                                                                                                                                                                                      Score 170; DB 3; Pred. No. 7.2e-22;
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APPLICANT: Nelestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: MODIFIED
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEG ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 22
LENGTH: 44
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 19
LENGTH: 44
                                   CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 44
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Application US/08955636A Patent No. 6017882
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Patent No. 6017882
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ORGANISM: Homo sapiens
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NAME/KEY: MOD_RES
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LOCATION: (0)...(
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OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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                       TYPE: PRT
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les 42; Conserv
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Pred. No. 1.6e-21;
0; Mismatches 2
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Pred. No. 1.6e-21;
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GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION UMBER: US/08/955,636A
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 25
LENGTH: 44
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US-08-955-636-25
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US-08-965-832-2
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Best Local
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Patent No. 5847085
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ORGANISM: Homo sapiens
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                                                                                  ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CHARLES T. ESMON AND MIKHAIL D. SMIRNOV TITLE OF INVENTION: Modified Protein C
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Local Similarity 90.9%;
             CLASSIFICATION: 530
WIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     STREET:
                                                APPLICATION NUMBER: US/08/965,832 FILING DATE: 7-NOV-1997
                                                                                                                                                                                                                                                                     STREET: Peachtree Street
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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CATION NUMBER:
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                                                                                                                                                                                                                                                                                     2: Patrea L. Pabst
2800 One Atlantic Center, 1201 West
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93.2%;
08/745,254
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Pred. No. 3.6e-20;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 160; DB 3; Length 44
Pred. No. 3.6e-20;
0; Mismatches '3; Indels
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US-08-295-411-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serine Pr
TITLE OF INVENTION: for Inhib
TITLE OF INVENTION: for Inhib
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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Best Local Similarity 90.9
Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/053,76
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REGISTRATION NUMBER: OMFF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873.8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 2:
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STRANDENNESS: sin-
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                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                         APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-AUG-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: /note= "where Xaa means gamma
OTHER INFORMATION: carboxylglutamic acid"
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Office of Patent Counsel, The Scripps ADDRESSEE: Research Institute STREET: 10666 No. 5679639th Torrey Pines Road, TPC CITY: La Jolla STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                       COUNTRY: U:
ZIP: 92037
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NAME: Fitting, Thom REGISTRATION NUMBER:
                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                                                                                                                                                                                                                                                                                                                             USA
                     Thomas
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90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine Protease-Derived Polypeptides Anti-Peptide Antibodies, Systems and for Inhibiting Coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "partial sequence of human protein
                                                                                                                                                                                 US/08/295,411
  34,163
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Pred. No. 3.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Therapeutic Methods
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US-08-955-471-1
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Best Local S
Matches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08955471
Patent No. 5968751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Griffi
FILING DATE:
CLASSIFICATION:
ATTORNEY_AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE_POCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: Region
LOCATION: 1..157
OTHER INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,471
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: TS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                               STREET: 100.
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LOCATION: 158..169
OTHER INFORMATION: /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION:
                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 92037
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Mesters, Rolf M.
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Anti-Peptide Antibodies, Systems and Therapeutic Methods
for Inhibiting Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Protein C Heavy Chain"
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                                                                                                                         08/295,411
                  TSRI263.0C1
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                                                         Matches
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acid
                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                   NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /
OTHER INFORMATION: !
                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                           NAME/KEY: Region
LOCATION: 170..419
OTHER INFORMATION:
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LOCATION: 1..157
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                                                                                                                                                                                                                                                            OTHER INFORMATION:
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                                                      31;
                 1 ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
1 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                 619-554-2937
                                                                     81.2%;
                                                                                                                                                                                     Peptide"
                                                                                                                              /note= "Protein C Heavy Chain'
                                                                                                                                                                                                                                                            /note= "Protein C Light Chain"
                                                                                                                                                                                                    /note= "Protein C Activation
                                                                                                                                                                                                                                                                                                                                                                                                                    ۳.
                                                       2;
                                                                     Score 160; DB 2;
Pred. No. 4.8e-19;
                                                          Mismatches
                                                          11;
                                                                                  Length 419;
                                                         Indels
                                                          0
                                                       Gaps
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Search completed: March 1, 2004, 10:12:21 Job time : 17.5 secs

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                         SPTREMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 1, 2004, 09:55:12; Search time 37.5 Seconds (without alignments) 370.208 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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197
1 ANSFLXXLRQGSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1017041 segs, 315518202 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                               sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_lant: *
sp_vrodent: *
sp_virus: *
sp_vertebrate: *
sp_vertebrate: *
sp_rvirus: *
sp_rvirus: *
sp_bacteriap: *
sp_archeap: *
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sp_phage:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	ው	ហ	4	w	6)	1	Result No.
99,5	101	101	101	101	103.5	105	107	107	109	115	118	118	134	140	151	Score
50.5	51.3	51.3	51.3	51.3	52.5	53.3	54.3	54.3	55.3	58.4	59.9	59.9	68.0	71.1	76.6	Query Match I
442	481	481	481	340	443	524	433	231	455	482	ទទ	55	460	460	456	Length
13	11	11	11	11	13	13	13	4.	u u	11	4.	4.	<u>بر</u>	11	Ø	BG
Q804X1	088947	Q99L32	054740	Q80Y26	08ЛНС9	Q7SXH8	Q804X5	Q8N2N6	Q7SY86	Q63207	Q8IXB5	Q8J002	924660	Q91WN8	Q9TTRO	10
Q804x1 fugu rubrip	088947 mus musculu	Q99132 mus musculu	O54740 mus musculu	Q80y26 mus musculu	Q8jhc9 brachydanio	Q7sxh8 brachydanio	Q804x5 gallus gall	Q8n2n6 homo sapien	Q7sy86 xenopus lae	Q63207 rattus norv		Q8j002 homo sapien	Q99pc6 mus musculu	Q91wn8 mus musculu	Q9ttr0 canis famil	Description

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CACMERO	000000	CANCEL	Q8JHD0	Q8IXC5	Q8K3U6	Q8IXD5	Q29094	100160	Q28994	Q804X2	Q95ND6	Q95ND7	Q61109	Q804X6	Q8T6I3	Q7Z7P3	Q15253	Q9NSD0	Q16519	Q7Z715	Q804W9	Q804W7	Q804X7	Q8NEK6	Q7T3B6	Q8JJ40	Q9GMD9	Q8JHC8	Q96PQ8
מטטוופס אינס המתרמס			brac	Q8ixc5 homo sapien	Q8k3u6 rattus norv	QBixd5 homo sapien	Q29094 sus scrofa	Q91001 gallus gall	s sn	fu	an t	ΪĐ	12	s gall	aloc	homo	Q15253 homo sapien	homo	homo	pomo s	9 fugn	Q804w7 fugu rubrip	gallu	Q8nek6 homo sapien	Q7t3b6 brachydanio			68	4 8

ALIGNMENTS

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IPR006209; EG	InterPro: IPR009003; Cys_Ser_trypsin.	erPro; IPR000152; Asx_hydroxy1_S.	GO:0006508; P:proteolysis and pe	GO:0004295; F:trypsin activity	GO:0008233;	GO:0004263; F:chymotrypsin activity	GO:0005509;	GO:0005576;	P; P04070; 1A	EMBL; AJ001979; CAA05126.1;	ы	37-238 (1999).	olymorphiams.	I., Kopp T.,	PubMed=10443005;	SEQUENCE FROM N.A.		Mamm. Genome 10:135-139(1999).		"Molecular characterization and chromosomal assignment of the canine		Kopp	UENCE FROM	[2] T		; Fissipedia; Canidae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	familiaris (Dog)	PROC.	2003 (Tremetret.	(TrEMBLrel. 13, Last	-2000 (TrEMBLrel. 13, Created)	Q9TTRO;	Q9TTRO PRELIMINARY; PRT; 456 AA.	TRO

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RESULT 2
Q91WN8
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                                                                                                                                                                        Matches
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Best Local :
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PIAM, PRO089; trypsin; 1.

PRINTS; PRO0722; CHYMOTRYPSIN.

PRINTS; PRO0701; GLABLOOD.

SMART; SMO0081; EGF; 2.

SMART; SM00081; EGF; 2.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS00010; ASX_HYDROXYL; 1.

PROSITE; PS00012; EGF 1; 1.

PROSITE; PS001187; EGF Ch; 1.

PROSITE; PS01187; EGF Ch; 1.

PROSITE; PS01187; EGF Ch; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_SER; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BROC.
Mus musculus (Mouse).
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; '
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TriMBLrel. 19, Created)
01-DEC-2001 (TriMBLrel. 19, Last sequence update)
01-DEC-2003 (TriMBLrel. 25, Last annotation update)
Similar to protein C.
                                                                                       InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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InterPro;
                          InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                       interPro;
                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28;
0006508; P:proteolysis and peptidolysis; IEA.

o; IPR000152; Asx hydroxyl S.

o; IPR001003; Cys Ser trypein.

o; IPR00181; EGF Ca.

o; IPR006209; EGF like.

o; IPR006239; GLA blood.

o; IPR001314; Peptidase S1.

o; IPR001314; Peptidase S1A.

o; IPR001294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain; Hydrolase; Protease;
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IPR001254; Peptidase_S1.
IPR001314; Peptidase_S1A.
IPR000294; VitK_dep_GLA.
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IPR006210; IEGF.
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195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6;
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PROTEIN C LIGHT CHAIN.

PROTEIN C CONNECTING DIPEPTIDE.

PROTEIN C HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 151; DB 6;
Pred. No. 3.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7AD3A8C1C34E59FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6; Length 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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RESULT
Q99PC6
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               ACOCCO COCCO COCCO
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MGD; MGI:97771; Proc.

GG; GG:0005576; C:extracellular; IEA.

GG; GG:0005509; F:calcium ion binding; IEA.

GG; GG:0005509; F:chymotrypsin activity; IEA.

GG; GG:0008233; F:peptidase activity; IEA.

GG; GG:0008233; F:peptidase activity; IEA.

GG; GG:0006206; F:trypsin activity; IEA.

GG; GG:0006506; F:proteolysis and peptidolysis; IE2

R [nterPro; IPR000152; Asx.hydroxyl S.

R InterPro; IPR000163; Asx.hydroxyl S.

R InterPro; IPR00184; EGF Ca.

R InterPro; IPR00184; EGF Ca.

R InterPro; IPR002383; GLA blood.

R InterPro; IPR001314; Peptidase S1.

R InterPro; IPR001314; Peptidase S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best
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PfAM; PF00099; trypsin; 1.

PFAM; PF00008; trypsin; 1.

PRINTS; PR00072; CHYMOTRYPSIN.

PRINTS; PR00072; GLAELOOD.

SMART; SM00019; EGF CA; 1.

SMART; SM00019; EGF CA; 1.

SMART; SM00020; Tryp SPC; 1.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS01186; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS001187; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00134; TRYPSIN SER; 1.

PROSITE; PS00134; TRYPSIN SER; 1.
Pfam; PF00008; EGF; 2.
Pfam; PF00089; 9la; 1.
Pfam; PF00089; trypein; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM000020; Tryp_SPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99PC6
Q99PC6;
01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases
-1-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26;
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Similarity 59.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain; Hydrolase; Protease; 460 AA; 51818 MW; 0117F2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (TramBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 17, (TrEMBLrel. 17, (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 140; DB 1:
Pred. No. 2.9e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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0117F26E68FCC274 CRC64;
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A Cho M., Dongchon K., Hamasaki N.;
T "Gene Analysis of Anticoagulation Pactors in Japanese Thrombotic
T Patients. Genetic Background of Thrombophilia in Japan.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL, AB08370; BAC21172.1;
R GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
InterPro; IPR000283; GLA blood.

R InterPro; IPR000284; GLA blood.

R InterPro; IPR000294; VitK_dep_GLA.

R FINTS; PR00001; GLABLOOD.

RR PRINTS; PR00001; GLABLOOD.
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Best Local Similarity
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PROSITE;
PROSITE;
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PROSITE;
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EGF-like
                                                            Q8IXB5;
01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8J002;
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                                                   Protein C (Fragment).
                                                                                                              Q8IXB5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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             Eukaryota;
                         Homo sapiens (Human)
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TE; PS00022; EEF [; 1.

TE; PS01186; EGF [2; 2.

TE; PS01187; EGF [CA; 1.

TE; PS01187; EGF [CA; 1.

TE; PS00011; GLU_CARBOXYLATION; 1.

TE; PS00014; TRYPSIN_DOM; 1.

TE; PS00135; TRYPSIN_HIS; 1.

TE; PS00135; TRYPSIN_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42
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                                                                                                                                                                                                  1 ANSFLXXLRQGSLXRXCIXXICDFXXAXXIFEDVDDT 37
                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                           ANSFLKELRHSSLERECIEEICDFEEAKEIFQNVDDT
    Eutheria;
                                                                                                                                                                                                                                                                           55 AA; 6527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 AA;
             Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                     55
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  Chordata;
Primates;
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                                                                                                                                                                                                                                     59.9%;
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23, Last sequence update)
25, Last annotation updat
                                                              23,
                                                              Last
Last
                                                                                       Created)
                                                                                                                                                                                                                         Pred. No. 1.7e-12;
2; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 134; DB 11
Pred. No. 3.1e-14
                                                                                                                                                                                                                                     Score 118; DB 4; Pred. No. 1.7e-12;
                                                                                                                                                                                                                                                                           4F89496534A78836 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                              sequence update)
annotation update)
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                                                                                                                                                                                                                                                  Length 55;
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                                                                                                                                                                                                                           Gaps
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RESULT 6
Q63207
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REGOPS; SO1.26; -...

REGO; GO:0005509; F:capticum ion binding; IEA.

REGO; GO:0004263; F:chymortypsin activity; IEA.

REGO; GO:0004263; F:peptidase activity; IEA.

REGO; GO:0006508; P:proteclysis and peptidolysis; IE/

REGOP; GO:0006508; P:proteclysis and peptidolysis; IE/

REGOP; GO:0006508; P:proteclysis and peptidolysis; IE/

REGOP; GO:0006509; REGOP; Ca.

REGOP; GO:0006509; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                               Carboxylase ";
Thromb. Res. "80:63-73(1995)
-!¹ SIMILARITY: BELONGS TO
EMBL; X79807; EXRT.
PIR; S49075; EXRT.
HSSP; P00742; 1XKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q63207;-
Q63207;-
Q1-NQV-1996
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PRINTS; PR00001; GLABLOX
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
MEDLINE=96093366; PubMed=8578539;
Stanton C., Ross R.P., Hutson S., Wallin R.;
"Evidence for competition between vitamin K."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intracellular processing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 ANSFLEELRHSSLERECIEEICDFEEAKEIFONVDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S (TrEMBLrel. 01, 5 (TrEMBLrel. 01, 01, 01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 AA; 6475 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           80:63-73(1995).
TY: BELONGS TO PEPTIDASE FAMILY S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118; DB 4
Pred. No. 1.7e-1
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3803696534BC9289 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vitamin K-dependent clotting
ne vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
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RESULT 7
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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T. Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko I., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Staplecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley R.C., Scherren E.J., Lu X., Gibbs R.A.,

RA Richards J.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Richards J.W., Sodergren E.J., Lu X., Gibbs R.A.,

RA Rahes J., Houton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and mittal analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CYMMOTRYPSIN.

PRINTS; PR00701; EGFELOOD.

PRINTS; PR00001; GFABLOOD.

PRINTS; SM00069; GLAF, 1.

SMART; SM00069; GLAF, 1.

SMART; SM00069; Tryp SPc; 1.

SMART; SM00069; GLAF, 1.

SMART; SM00069; GLAF, 1.

SMART; SM00022; EGF 1; 1.

PROSITE; PS00116; ASX HYDROXYL; 1.

PROSITE; PS01186; EGF 2; 2.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01011; GLU CARBOXYLATION; 1.

PROSITE; PS000134; TRYPSIN DOM; 1.

PROSITE; PS000134; TRYPSIN SER; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.

Kenopus laevis (African clawed frog).

Kenopus laevis (African clawed frog).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q7SY86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus.
mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSFFEEIKKGNLERECVEEICSFEEAREVFEDNEKTTEFWNKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225:384~391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protease; Serine protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0284678E3954A698 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 6
Q8N2N6
   Q804X5
AC Q80
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR002383; GIA blood.
InterPro; IPR002094; Vitk_dep_GIA.
Pfam; PF00594; gla; 1.
PRINTS; PR000001; GIABICOD.
SMART; SM00069; GIA; 1.
SMART; SM00069; GIA; 1.
SMART; PS00011; GIU CARBOXYLATION; 1.
ENOSTART; PS00011; GIU CARBOXYLATION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOGAI T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; "NEDO human CDNA sequencing project.", "NIDO human CDNA sequencing project.", Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases
EMBL; BC054968; AAH54968.1; -.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vert
Archosauria; Aves; Neognathae; Galliformes;
                                                                                                                             01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anticoagulant protein C precursor (EC 3.4.21.69).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein. SEQUENCE 231 AA; 25844 MW; 8A373B0D5C1D0D81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein FLJ90093.
Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Whole;
                                                                                                                                                                                                                                                                                                      Q804X5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AK074574; BAC11069.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rocar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 ANEFLEELROGTIERECMEEICSYEEVKEVFENKEKTMEFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AFNFMEELKPGSLERECIEEKCDFEEAFEIFETKEDTLNEWAKY 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.3%;
                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107; DB 4;
Pred. No. 6.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 109;
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
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Phasianidae;

Phasianinae;

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Q7SXH
Q7SXH
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D7 01-0C
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GO; GO:0004263; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:00016787; F:hydrolase activity; IEA.
GO; GO:0004898; F:protein C (activated) activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000152; Asx_hydroxyl_s.
InterPro; IPR00903; Cys_Ser_trypsin.
InterPro; IPR000742; EGF_Ca.
InterPro; IPR000209; EGF_Ci.
InterPro; IPR002209; EGF_Ci.
InterPro; IPR002209; EGF_Ci.
InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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PEAM; PRO0795; TYPSIN; 1.

PRINTS; PRO0701; GLABLCOD.

SMART; SM00119; EGF; 2.

SMART; SM00119; EGF; 2.

SMART; SM00101; EGF; 1.

SMART; SM00100; GLA; 1.

SMART; SM00000; TYPS SPC; 1.

SMART; SM00000; TYPS SPC; 1.

PROSITE; PS00101; ASK; HYDRXYL; 1.

PROSITE; PS01186; EGF=1; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; GLU CARBOXYLATION; 1.

PROSITE; PS0134; TRYPSIN_HS; 1.

PROSITE; PS0134; TRYPSIN_HS; 1.

PROSITE; PS0135; TRYPSIN_HS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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"Comparative sequence analysis and molecular evolution o coagulation genes from Gallus gallus and Fugu rubripes." Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AF465270; AA033365.1; ---
EMBL; AF465270; AA033365.1; ---
EMBL; AF465270; Cextracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q7SXH8;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                Hypothetical protein.

Brachydanio rerio (Zebrafish) (Danio rerio).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Actinopterygii, Neopterygii; Teleostei, Ostariophysi, Cypriniformes;

Cyprinidae, Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q7SXH8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00008; EGF;
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                                                 SEQUENCE FROM N.A.
TISSUE=Body;
    MEDLINE=22388257; PubMed=12477932;
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                   CBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 AA; 48689 MW; E09DDEE56D7DA2A3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524
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    A COCCEPTION AND READER AND COCCEPTION AND COCCEPTI
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RA Klausner R.D., Colline F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Mcore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richarde S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holtinge A.C., Grimwood J., Schmutz J., Myers R.M., Butkerfield Y.S.,
RA Krzywinski M.I., Skaiska U., Smailus D.E., Schnerch A., Schein J.S.,
RA Annes S.J., Marry M A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBJHC9;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
Coagulation factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC055596; AAH55596.1; -.
                                                                                    InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Hanumanthalah R., Day K., Jagadeeswaran P.;
"Comprehensive analysis of blood coagulation pathways in Teleostei:
Evolution of coagulation factor genes and identification of zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISSUE=Body;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 ANTVFEELKPGNLERECVEEICDHEEAREVFERVDKTEIFWAKY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 53.3%; Score 105; DB 13;
Similarity 43.2%; Pred. No. 3.4e-09;
o; IPR009003; Cys_Ser_trypsin.
c; IPR000742; EGF_Ca.
c; IPR001881; EGF_Ca.
c; IPR006209; EGF_like.
c; IPR006239; GLAF_blood.
c; IPR006210; IEGF_.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REDILINE-22386257; PubMed=12477932;

REDILINE-22386257; PubMed=12477932;

RESTRUBBERG R.L., Feingold R.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA History M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

RA Pahey J., Helton E., Kettenan M., Madan A., Rodrigues S., Sanchez A.,

RA History M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,

RA Hones S. T., Marra M.A., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Korywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Korywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Korywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piam; PRO0094; gla; 1.

Piam; PRO0094; trypsin; 1.

Piam; PRO0094; trypsin; 1.

PRINTS; PRO072; CHYMOTRYPSIN.

PRINTS; PRO0701; GLABLOOD.

SMART; SM00181; EGF; 2.

SMART; SM00181; EGF; 1.

SMART; SM00020; Tryp, SPC; 1.

SMART; SM00020; Tryp, SPC; 1.

PROSITE; PS01186; EGF-2; 2.

PROSITE; PS01186; EGF-2; 2.

PROSITE; PS00114; GLU CARBOYLATION; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

EGG-11ke domain; Hydrolase; Procease; Seriese; Serie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q80Y26;
Q80Y26;
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GIA.
Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC050219; AAH50219.1; -.
GO; GO:0005576; C:extracellular; IBA.
GO; GO:0005509; F:calcium ion binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                          Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omain; Hydrolase; Protease; Serine protease. 443 AA; 48823 MW; 2D2504718AE94FF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
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RESULT 13
054740
             ALGORAR RESERVATOR OF A RESERVATION OF A
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Best Local
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GO; GO:0006508; P:proteolysis and peptidol
InterPro; IPR009152; Asx hydroxyl S.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR001881; EGF II.
InterPro; IPR001438; EGF II.
InterPro; IPR001438; EGF II.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
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Pfam; PF00594; gla; 1.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00001; GLABLOOD.
SMART; SM00179; EGF CA; 1.
SMART; SM00069; GLA; 1.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0004804; F:blood coagulation factor X activity; IEA.
GO; GO:0003804; F:blood coagulation factor X
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0006233; F:peptidase activity; IEA.
GO; GO:0006295; F:trypsin activity; IEA.
GO; GO:0006508; P:protecolysis and peptidolysis; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR009003; Cys_Ser_trypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEWBLrel. 06, Created)
01-JUN-1998 (TrEWBLrel. 06, Last sequence update)
01-JCT-2003 (TrEWBLrel. 25, Last amnotation update)
Coagulation factor X precursor (EC 3.4.21.6).
                                                                                                                                                                                                                                                                                                                                                                    -!-, SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AJ222677; CAA10933.1; -.
HSSP; P00742; IXXA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heidtmann H.H., Kontermann R.E.; "Cloning and recombinant expression of mouse coagulation factor Thromb. Res. 92:33-41(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00010; ASK HYDROXYL; 1.
PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pBluescript.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F10 OR FA10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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InterPro; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98454993; PubMed=9783672;
                                                                                                                                                                                                                                                                                                                  MGI:103107; F10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS00011; GLU CARBOXYLATION;
PS50240; TRYPSIN DOM; 1.
PS00134; TRYPSIN HIS; 1.
340 AA; 38359 MW; EE252I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.3%; Score 101; DB 1 38.6%; Pred. No. 1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EE252D6157720811 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptidolysis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 11; Length
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RESULT 14
Q99L32
ID Q99L3
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MSEROPS; 801.216; -..

MEROPS; 801.216; -..

MGD; MGI:103107; F10

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0005509; F:calcium ion binding; IEA.

GO; GO:0004233; F:chymotrypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006083; P:proteclysis and peptidolysis; IEA.

InterPro; IPR000152; Asx. hydroxyl_S.

InterPro; IPR000152; Asx. hydroxyl_S.

InterPro; IPR0001438; EGF_Ca.

InterPro; IPR001438; EGF_Ca.
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PÉAM; PPO00894; 91a; 1.

PÉAM; PPO00894; 91a; 1.

PÉAM; PPO0089; CYPANOTRYPSIN.

PRINTS; PRO0010; EGFPLOOD.

PRINTS; PRO0010; EGFPLOOD.

PRINTS; PRO0010; EGF CA; 1.

SMART; SM00020; GLA; 1.

SMART; SM00020; TYPP SPC; 1.

PROSITE; PS00010; ASX HYDROXYL; 1.

PROSITE; PS00186; EGF 1; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS01187; EGF CA; 1.

PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_DIS.

PROSITE; PS00135; TRYPSIN_DIS.

PROSITE; PS00135; TRYPSIN_DIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Q99132;
Q99132;
Q1-JUN-2001
Q1-JUN-2001
Q1-CCT-2003
                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BC003877; AAH03877.1; -.
HSSP; P00742; IXKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                               Coagulation factor X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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o; IPR001881; EGF_II.
o; IPR001383; EGF_II.
o; IPR00239; EGF_like.
o; IPR002383; GLA_blood.
o; IPR001384; Peptidase_S1.
o; IPR001314; Peptidase_S1A.
o; IPR000294; VitK_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANSFFEEFKKGNIERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain; Hydrolase; Protease; Serine protease;
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COAGULATION FACTOR X.
; CF702DE5EF9D97AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AA
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                                                                                                                                                                                                                                                                                                                                                                                            update)
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RESULT 15
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SMART; SM00069; GLA; 1.

SMART; SM00020; Tryp SPC; 1.

SMART; SM00020; Tryp SPC; 1.

PROSITE; PS001010; ASX HYDROXYL; 1.

PROSITE; PS00122; EGF 1; 1.

PROSITE; PS00122; EGF 2; 2.

PROSITE; PS00136; EGF 2; 2.

PROSITE; PS00131; GLU_CARBOXYLATION; 1.

PROSITE; PS00131; GLU_CARBOXYLATION; 1.

PROSITE; PS00135; TRYPSIN DOM; 1.

PROSITE; PS00135; TRYPSIN SER; 1.
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InterPro; IPR002383; GLA blood.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR000194; VitK_dep_GLA.
Pfam; PP000008; EGF; 2.
Pfam; PP00594; Gla; 1.
Pfam; PP00594; Gla; 1.
Pfam; PP00089; trypsin; 1.
PRINTS; PR00012; CHYMOTRYPSIN.
PRINTS; PR00012; EGFBLOOD.
PRINTS; PR00001; GLABLOOD.
                                                                                             MEROPS; S01.216; -...
MGD; MGI:103107; F10.
MGD; GO:0005576; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0005509; F:chymotrypsin activity; IEA.
GO; GO:0004263; F:chypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                Liang Z., Cooper A., DeFord M.E., Carmeliet P., Collen D.,
Castellino F.J., Rosen E.D.;
"Cloning and characterization of a cDNA encoding murine coagulation
factor X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          088947;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                   STRAIN-129SJ;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Thromb. Haemost. 80:87-91(1998).
                                                                                                                                                                                                                                                                                                                   MEDLINE=98347933;
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    PubMed=9684791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.3%; Score 101; 38.6%; Pred. No. :
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DR GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

DR InterPro; IPR000132; Asx.hydroxyl S.

DR InterPro; IPR000132; Asx.hydroxyl S.

DR InterPro; IPR000303; Cyg-Ser_trypsin.

DR InterPro; IPR001081; EGF_Ca.

DR InterPro; IPR001244; Peptidase_Sl.

DR InterPro; IPR001234; Peptidase_Sl.

DR Pfam; PP00594; Glaf; L.

DR Pfam; PP00594; Glaf; L.

DR PRINTS; PR00101; GLABLOOD.

DR PRINTS; PR00101; GLABLOOD.

DR PRINTS; PR00101; GLABLOOD.

DR PROSTIE; P800101; GLABLOOD.

DR PROSTIE; P800116; EGF_CA; L.

DR PROSTIE; P800115; TRYESIN_SER; L.

DR PROSTIE; P800116; EGF_CA; L.

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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March 1, 2004, 10:01:28 ; Search time 28 Seconds
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331.812 Million cell updates/sec
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197
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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461	461	461	419	419	419	44	419	419	419	419	419	419	419	419	Length
15	14	10	15	14	10	14	15	15	14	14	14	15	15	14	B
US-10-168-407-2	US-10-182-263-2	US-09-978-917A-2	US-10-168-407-1	US-10-182-263-1	US-09-978-917A-4	US-10-298-330-1	US-10-168-407-4	US-10-168-407-3	US-10-182-263-5	US-10-182-263-4	US-10-182-263-3	US-10-168-407-6	US-10-168-407-5	US-10-182-263-6	ID
Sequence 2	Sequence 2	Sequence 2	Sequence 1	Sequence 1	Sequence 4	Sequence 1	Sequence 4	Sequence 3	Sequence 5	Sequence 4	Sequence 3	Sequence 6	Sequence 5	Sequence 6	Description
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; Sequence 5, Application US/10168407; Publication No. US20030207435A1; GENERAL INFORMATION:

US-10-168-407-5 RESULT 2

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-10-188-495-4	-10-189-123-40	0	-10-188-495-4	-10-189-123-4	-09-759-130B-	-10-188-495-4	-10-189-123-4	-09-759-130B-	-10-298-330-22	-10-298-330-2	-10-298-330-	-10-298-330-2	-10-360-101-	-10-386-89	-10-281-727-	-10-255-032-	-10-109-498-	-09-782-587B	-10-298-33	-10-375-741-	-10-017-122-	-10-383-898-	-09-782-587B	-10-038-854-9	-10-298-330-	-10-407-123-2	-10-348-504-4	-10-360-101-2	-10-298-330-
40, App	40,	Seguence 310, App	42	42, App	311	43, App	43	: 313, Ap	22	25, App	e 4, Appl	23	e 225, Ap	e 7, Appl	: 1, Appl	ı, Appl	e 1, Appl	e 1, Appl	ω	: 14, App	2, Appl	e 1, Appl	e 3, Appl	e 97, App	: 18, App	27, App	9 44, App	23	2,

ALIGNMENTS

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Sequence 6, Application US/10182263 (063)
Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
CURRENT ETILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
                                                                                                                                           ; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-6
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                                                                       Matches
                                                                                 Query Match
Best Local Similarity
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                                                                       35,
ANSFLEELROGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                       Conservative
                                                                     90.9%; Score 179; DB 14; Length 419; 79.5%; Pred. No. 3.9e-22; Indels (tive 0; Mismatches 9; Indels
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Sequence 6, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
                                                           FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/18199
PRIOR APPLICATION NUMBER: 60/189199
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
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US-10-182-263-3
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CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10182263 Publication No. US20030022354A1 GENERAL INFORMATION:
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Best Local :
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APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
                                                                                                                                                                                                                                                                                           APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTBIN C DERIVATIVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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Sequence 4, Application US/10182263
Rabbication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
FITTLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
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US-10-182-263-4
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                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/10182263
Publication No. US20030022354A1
GENERAL INFORMATION:
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Best Local Similarity
Matches
                  Query Match 88.3%; Score 174; DB 14; Length 419; Best Local Similarity 77.3%; Pred. No. 2.8e-21;
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Best Local (
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PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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77.3%;
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ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH

US-10-168-407-3

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-4
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                                                                                                                                                                               ; Sequence 1, Application US/10298330 ; Publication No. US20030100506A1 ; GENERAL INFORMATION;
                                                                                                                                                                                                                                                 US-10-298-330-1
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Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Jones, Bryan E
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The Local Similarity
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Publication No. US20030207435A1
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APPLICANT: Jones, Bryan B
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILLING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
APPLICANT: Nelsestuen, Gary L.
TITLE OF INVENTION: Modified Vitamin K-Dependent
TITLE OF INVENTION: Modified Vitamin K-Dependent
TITLE OF INVENTION: MODIFIED VITABLE
FILE REFERENCE: 09531-127001
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/497,591
PRIOR FILING DATE: 2000-02-03
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TYPE: PRT
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GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruan E

TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 419
TYPE: PRT
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PRIOR FILING DATE: 1999-04-29
PRIOR FILING DATE: 1997-10-23
PRIOR FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FASTESEQ FOR WINDOWS Version 4.0
SEQ ID NO 1
LENGTH: 44
TYPE: PRI
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APPLICANT: Maxygen Aps; Maxygen Holdings
APPLICANT: Maxygen Aps; Maxygen Holdings
TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 419
TYPE: PT
ORGANISM: Homo sapiens
US-09-978-917A-4
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FBATURE:
NAME/KEY: VARIANT
LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29
OTHER INFORMATION: Xaa = gamma carboxyglutamic or glutamic acid
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70.5%; Pred. No. 7e-19;
ative 2; Mismatches
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CURRENT APPLICATION NUMBER: US/10/168,407; CURRENT FILING DATE: 2002-11-04; NUMBER OF SEQ ID NOS: 12; SOFTWARE: PatentIn version 3.1; SEQ ID NO 1; LENGTH: 419; TYPE: PRT; ORGANISM: Homo sapiens
US-10-168-407-1
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US-10-168-407-1
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US-09-978-917A-2
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                                                                                                                                                        ; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (43)...(461)
US-09-978-917A-2
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TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0.219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09978917A Publication No. US20030027299A1 GENERAL INFORMATION:
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Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X.13610
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Best Local Similarity 70.5
Matches 31; Conservative
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                                                                                                                                                                                                                                   NAME/KEY: SIGNAL LOCATION: (1)...(42)
                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                       ENGTH: 461
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43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 86
                              1 ANSFLXXLRQGSLXRXCCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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31; Conserv
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70.5%; Pred. No. 7e-19;
ative 2; Mismatches
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70.5%;
                                                                                                81.2%; Score 160; DB 10; Length 461; 70.5%; Pred. No. 7.8e-19;
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Sequence 2, Application US/10168407

Publication No. US20030207435A1

GENERAL INFORMATION:

APPLICANT: Gerlitz, Bruce E

APPLICANT: Jones, Bryan E

TITLE OF INVENTION: PROTEIN C DERIVATIVES

FILE REFERENCE: X-13610

CURRENT APPLICATION NUMBER: US/10/168,407

CURRENT FILING DATE: 2002-11-04

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REPERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182/263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR APPLICATION NUMBER: 60/189199
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOSTWARE: Patentin version 3.1
SEQ ID NO 2
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                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-407-2
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US-10-168-407-2
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-263-2
Search completed: March 1, 2004, 10:11:10
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Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
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Local Similarity 70.5%; Pred. No. 7.8e-19;
nes 31; Conservative 2; Mismatches 11; Indels
                                                                       43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 86
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                                                                                                                      1 ANSFLXXLROGSLXRXCIXXICDFXXAXXIFEDVDDTLAFWSKH 44
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                                                                                                                                                                                              Similarity
                                                                                                                                                                   81.2%; Score 160; DB 15; Length 461; 70.5%; Pred. No. 7.8e-19; tive 2; Mismatches 11; Indels
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Minimum DB seq length: 0
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Copyright (c) 1993 - 2004 Compuç
geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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Pred. No. d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	B	ID	Description
, Н	180	90.9	44	2	AAY18297	Aay18297 Modified
N	176	88.9	Ë	4	826	Ď82676 Human p
ω	176	٠	₽	4	8267	2675 Human pr
4.	176		\vdash	4	Ø	628 Human
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ტ	176	8	н	4	0862	Human
7	174	.7	45	ຫ	7995	9950 Human pr
œ	172	ς,	44	N	AAY18299	299
w	172	٠,	44	N		18309
10	172	σ.	44	N	AAY18298	
11	172	ა	44	N	AAY18303	8303
12	172	9	44	4	AAB36402	Aab36402 Human pro
13	172	٥,	44	7	ADD50094	0094 Human
14	172	9	45	N	AAW75710	Aaw75710 Partial h
15	172	'n	45	m	ABB79947	
16	172	٥.	45	7	ADB71155	Human
17	172	9	415	w	AAY56803	Trunca
18	172	9	419	N	AAR35760	760
19	172	9	419	N	275	753 Primary
20	172	σ,	419	4.	AAB82673	673
21	172	9	419	4	AAB36896	Aab36896 Human pro
22	172	9	419	4.	œ	Aab36897 Human pro
23	172	9	419	4	w	898 Human
24		9	419	4.	AAB36894	94 Human
25	~ J	9	419	4.	AAE08625	Aae08625 Human mat

This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protesin which has enhanced membrane binding affinity as compared to the native protein

Claim 6; Page 78; 86pp; English.

Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.

WPI; 1999-288309/24.

Nelsestuen

(MINU) UNIV MINNESOTA.

45	44	43	42	41	40	3 9	3 8	37	36	3 5	ω 4.	ω ω	32	31	30	29	28	27	26
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Aau99097	Aau99088	Aau99076	Aau99050	Aau99047	Aau99039	Aau99033	Aau99021	Aau99012	Aau99084	Aau99083	Aau99072	Aau99063	Aau99049	Aau99037	Aau99026	Aau99018	Aau99008	Aau99006	Aau99005
Human																			
Dro	Pro																		

ALIGNMENTS

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RESULT 1
AAY18297
ID AAY1
key Location/Qualifiers Misc-difference 1. .44
                                                                                                                                                                                                                    Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                              GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                     AAY18297;
                                                                                                                                23-OCT-1997;
                                                                                                                                             20-0CT-1998;
                                                                                                                                                                       WO9920767-A1.
                                                                                                                                                                                                                                       tnerapy.
                                                                                                                                                                                                                                                           Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                        17<sub>7</sub>AUG-1999
                                                                                                                                                                                                                                                                                                   AAY18297 standard; peptide; 44 AA.
                                                                                                                                                          29-APR-1999.
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                97US-00955636.
                                                                                                                                             98WO-US022152.
                                                                                                                                                                                    acid"
                                                                                                                                                                                          /note= "Xaa= gamma-carboxyglutamic acid,
                                                                                                                                                                                           or glutamic
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AABB2677 & AABB2677 & AABB2677 & AABB2677 & AABB267 & AA
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Best Local
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Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anticoagulant; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-2001
                      Cleavage-site
                                                                                           Peptide
                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                             Disulfide-bond
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                      zymogen"
169. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                             /note= "cleavage makes a 2-chain inactive precursor amino acid light chain attached via a disulfide bond 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylated"
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
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169. .170
/note= "thrombin cleavage site"
                                                                       /note= "activation
                                                                                                                                                                                                                                                                                                                                                                                               /note= "Gln in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "gamma-carboxylated'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                                    'note= "Asn in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note=
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100.0%; Pr
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                                                                    peptide;
                                                                         removal activates the 2-chain
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The present sequence is that of a claimed human protein C derivative in cc which Ser at position 11 of the mature wild-type protein C sequence (see CABS2673) is substituted with Gly, Gln at position 32 with Glu, Asn at CC position 33 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention C 254 with Ser. It is an example of protein C derivatives of the invention C that have at least 2 amino acid substitutions, but which have increased CC with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the biological activity of CC trembinant DNA methods is claimed. The protein C derivatives are useful C for treating coronary syndromes and disease states predisposing to CC thrombosis (e.g. myocardial infarction and unstable angina) vascular CC cochistive disorders and hypercoagulable states, sepsis (in combination CC pathway inhibitor), thrombotic disorders (in combination with an anti-CC platelet agent or by local delivery through an intracoronary catheter), CC protein C deficiency, acute arterial thrombotic occlusion, or stenosis in coronary, cerebral or peripheral arteries CC or in vascular grafts. Human patients with genetically predisposed CC prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-2000; 2000US-0179801P
14-MAR-2000; 2000US-0189197P
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 53-54; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAH26364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerlitz BE, Jones BE
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Sequence 419 AA;
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196. .212
248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-glycosylated"
331. .345
356. .384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylated"
329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Thr in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein"
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AAB82675
                                                          RESULT 3
AAB82675;
                            AAB82675 standard; protein; 419
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ß Ś

Query Match Best Local Matches

Local Similarity

34;

Conservative

88.9%;

Score 176; DB 4; Pred. No. 1.9e-20; 0; Mismatches 10

10;

0

Gaps

0;

Length 419; Indels

1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH

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Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal;
                                                                                                                                                                                                                                                                Disul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human protein C derivative (S11G/Q32E/N33D/L194S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-0CT-2001
                                                                                                                                                                                                                                            Cleavage-site
                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticoagulant; therapy; mutant; mutein.
19-JAN-2001; 2001WO-US000020
                                       WO200157193-A2
                                                          Disulfide-bond
                                                                  Disulfide-bond
                                                                                      Modified-site
                                                                                                         Modified-site
                                                                                                                            Modified-site
                                                                                                                                     Disulfide-bond
                                                                                                                                                        Misc-difference
                                                                                                                                                                           Cleavage-site
                                                                                                                                                                                                                                                                           Disulfide-bond
                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                               Disu.
                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                       sulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                  /note=
29
                                                                 /note= "N-glycosylated"
                                                                                                                                                                                                                156. 157

/note= "cleavage makes a 2-chain inactive precursor amino acid light chain attached via a disulfide bond 262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                           /note= "Gln in wild-type protein" 33
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
19
                                                                                                                                    196. .212
                                                                                                                                                                                  zymogen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                             note= "activation peptide; removal
                                                                                                                                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                 note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                              'note= "N-glycosylated"
                                                                                                                                              'note= "Leu in wild-type protein"
                                                                                                                                                                  'note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                "Asn in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                      "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                          "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                    "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Gla domain"
                                                                                                                                                                                                                                                                                                                                                                                             "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                               "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "gamma-carboxylated"
                                                                                                                                                                                               activates the 2-chain
                                                                                                                                                                                                                            bond to
                                                                                                                                                                                                                                     (155-
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The present sequence is that of a claimed human protein C derivative in CC which Ser at amino acid position 11 of the mature wild-type protein C sequence (see AAB82673) is substituted with Gly, Gln at position 32 with CC Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. The CP protein is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased CC with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the biological activity of CP treating coronary syndromes and disease states predisposing to CP trombosis (e.g. myocardial infarction and unstable angina) vascular CC with bactericidal permeability increasing protein or with tissue factor CC with bactericidal permeability increasing protein or with tissue factor CC platelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed CC prothrombotic disorders may be treated by gene therapy (all claimed)
  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human protein C derivative for treating, einfarction, unstable angina, sepsis, thrombotic thrombotic occlusion, and thromboembolism.
                                                         Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-2000; 2000US-0179801P.
14-MAR-2000; 2000US-0189197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 52-53; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH26363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EFIL ) LILLY & CO ELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-496919/54.
  Similarity
                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones BE;
88.9%;
  Score 176;
Pred. No. 1
  DB 4;
.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e.g., myocardiai
c disorders, acute arterial
                   Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myocardial
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AAE08628
                                                                                                              Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hyperroosqulable state; angina, sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                       Human protein C derivative #2.
                                                                                                                                                                                                                                                                                                                                                            AAE08628 standard; protein; 419 AA
                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                                                                                            AAE08628;
                                                                                                                                                                                                                                                                                         (first entry)
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16-AUG-2001

WO200159084-A1

뮍 S

Matches

34;

Conservative

<u>.</u>.

Mismatches

10;

Indels

0

Gaps

0

44 44

1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH

ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH

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ARESULT 5
AAE08627
ID AAE0
XX AAE0
AC AAE0
XX DT 01-N
XX Huma
XX Honc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human protein C derivatives and nucleic acid complexules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased continuity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the current of acute coronary syndromes e.g. myocardial infarction and cunstable angina; and disease states predisposing to thrombosis; vascular coclusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, csickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing protein c deficiency; acute arterial thrombotic occlusion, thrombotic disorders in combination with an anti-platelet agent; thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 34
                                                                                                                                            Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angian; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; vital haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                                                                                  Human protein C derivative #1.
                                                                                                                                                                                                                                                                                                                                                           01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-2001; 2001WO-US001221
                                                               WO200159084-A1
                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                      AAE08627
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE08627 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIL )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 77.
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 47-48; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grinnell BW,
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2000US-0189199P.
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 176; DB 4;
Pred. No. 1.9e-20;
O; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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16-AUG-2001

/note= "Encoded by CAA'

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RESULT 6
AAE08629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human protein C derivatives and nucleic acid CC molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased control of the manufacture of and increased to the state of the protein C, and creatins the biological activity of the wild type protein C. Protein C derivatives are useful in the manufacture of a medicament for the collection of acute coronary syndromes e.g. myocardial infarction and cunstable angina, and disease states predisposing to thrombosis; vascular coclusive discorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, creating thrombosic discorders in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; coron vascular grafts in combination with a thrombotic agent. Nucleic acid molecules of the invention are useful for treating humans with combined sequence is human protein C derivative by gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                      vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thrombotism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                              Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction
                                                                                                                                                                                                                                                                Human protein C derivative #3.
                                                                                                                                                                                                                                                                                                     01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                           AAE08629 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-2000; 2000US-0181948P
14-MAR-2000; 2000US-0189199P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-2001; 2001WO-US001221
                                  Misc-difference
                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          AAE08629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 46-47; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Loca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRHSSLXXXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 77.3
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grinnell BW,
                                                                                                                                                                                                                                                                                                       (first entry)
                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 176; DB 4;
Pred. No. 1.9e-20;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                               infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human protein C derivatives and nucleic acid CC molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased CC sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein CC derivatives are useful in the manufacture of a medicament for the CC treatment of acute coronary syndromes e.g. myocardial infarction and constable angina; and disease states predisposing to thrombosis; vascular CC coclusive disorders and hypercoagulable states e.g. disseminated CC intravascular coagulation (DIC), burns, transplantations, thalassaemia, CC sickle cell disease, viral haemorthagic fever and haemolytic uremic CC syndrome; sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; CC protein; cheficiency; acute arterial thrombotic occlusion, thrombotic in combination with a thrombotic agent. Nucleic CC acid molecules of the invention are useful for treating humans with CC genetically predisposed prothrombotic disorders by gene therapy. The CC protein sequence is human protein C derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 48-49; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-FEB-2000; 2000US-0181948P.
14-MAR-2000; 2000US-0189199P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2001
                                                                                                                                  Protein C; Gla domain; human; blood clotting; anticoagulant; thrombolytic; antiarteriosclerotic; cardiant; antiaggregant; mutant;
                                                                                                                                                                                                                                                          ABB79950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substitutions at specified amino acid positions.
                Misc-difference
                                                                   Synthetic
                                                                                                                                                                                      Human protein C mutated Gla domain SED
                                                                                                                                                                                                                        12-DEC-2002
                                                                                                                                                                                                                                                                                           ABB79950 standard; protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200159084-A1
                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001-514662/56
DB; AAD15227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                 1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grinnell BW,
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                                                                                                                                                                                                                        (first entry)
                             Location/Qualifiers
/note= "wild-type Asp substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 176; DB 4;
Pred. No. 1.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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AAY1829 AAY1829 ID AAY1 XX AAY1 AC AAY1 XX AAY1 XX DT 17-A XX Modi XX Modi XX GLA XW GLA XW GLA XX Homo

17-AUG-1999 AAY18299;

(first entry)

AAY18299 standard; peptide; 44 AA

Homo sapiens

therapy.

GLA domain; mutein; vitamin K-dependent protein; clotting disorder;

Modified GLA domain of vitamin K-dependent protein

융 Ś

Matches Query Match Best Local :

1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

ANSFLEELRHSSLERECIEBICSFEEAKEIFEDVDDTLAFWSKH

Local 34;

Similarity

87.9%; 77.3%;

Conservative

0

Score 174; DB 5; Pred. No. 3.6e-21; 0; Mismatches 10

Length 45; Indels

0,

Gaps

0

Sequence 45 AA;

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amino acid substitutions. A preferred mutant (designated QCNSEDY, see CC ABB79946) has the mutations H10Q, S11Q, S12N, D32S, Q32E, N33D and H44Y, CC ABB79946) has the mutations H10Q, S11Q, S12N, D32S, Q32E, N33D and H44Y, CC and shows greatly enhanced anticoagulant activity in standard in vitro CC coagulation assays. The present mutant (designated SED) was produced in an example from the invention as a step toward the production of the CC QGNSEDY mutant Gla domain, and shows little, if any, improvement in CC anticoagulant activity over wild-type activated protein C. The invention CC provides methods for producing the variants based on DNA technology, and CC with the use of the variants for the treatment of coagulation disorders such as thrombosis or APC resistance, or in diagnostic test systems for CC assaying components of the protein C-anticoagulant system (all claimed). CC The variants may also be used in treating arteriosclerosis, myocardial CC infarction, and disseminated intravascular coagulation. Note: The present CC sequence is not shown in the specification but is derived from the human CC wild-type Gla domain sequence given on page 7 of the specification (see
                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is the protein sequence of a mutated Gla domain (N-terminal amino acids 1-45) of human protein C. The mutated Gla domain contains the substitution mutations D235, Q32E and M33D. Protein C and activated protein C variants comprising a mutated Gla domain are provided by the invention. The variants contain at least 6, and optionally 7-10, by the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New variant blood coagulation component, useful for manufacturing a medicament for treating or preventing coagulation disorders, e.g. thrombosis, comprises an anticoagulant activity in the protein C-anticoagulant system of blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001; 2001US-0272466P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-713449/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TACT-) TAC THROMBOSIS & COAGULATION AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002; 2002WO-SE000363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200270681-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "wild-type Asn substituted by Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note=
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RESULT 9
AAY18309
ID AAY1
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Best Local S
Matches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key Location/Qualifiers Misc-difference 1, .44
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nelsestuen GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09920767-A1
                                                                                                                                                                                                        Modified GLA
                                                                                                                                                                                                                                                      AAY18309,
                                                                                                                                                                                                                                                                            AAY18309 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Page 78; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
           20-OCT-1998;
                                 29-APR-1999
                                                       W09920767-A1
                                                                                                   Misc-difference
                                                                                                                                     Synthetic.
                                                                                                                                                Homo sapiens
                                                                                                                                                                       therapy.
                                                                                                                                                                                 GLA domain;
                                                                                                                                                                                                                               17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1999-288309/24
                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                     ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                     ANSFLXXLRESSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                  mutein;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                        domain of vitamin K-dependent protein.
                                                                                                                                                                                                                              (first
           98WO-US022152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00955636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98WO-US022152.
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid"
                                                                               acid"
                                                                                         'note= "Xaa=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Xaa= gamma-carboxyglutamic acid, or glutamic
                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                  vitamin K-dependent protein; clotting
                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                           97.7%;
                                                                                                                                                                                                                                                                              44
                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                       gamma-carboxyglutamic acid, or glutamic
                                                                                                                                                                                                                                                                                                                                                                                Score 172; DB 2;
Pred. No. 7.6e-21;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                       Length 44;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                   disorder;
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 10
AAY18298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                                                                                                                                                                                                                                                                                                  Modified GLA domain of vitamin K-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
                                                                                           Nelsestuen GL
                                                                                                                                                                20-OCT-1998;
                                                                                                                                                                                      29-APR-1999.
                                                                                                                                                                                                             WO9920767-A1.
                                                                                                                                                                                                                                                           Misc-difference 1.
                                                                                                                                                                                                                                                                                            Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                         GLA domain;
                                                                                                                                                                                                                                                                                                                                                                                                                AAY18298;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY18298 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 79-80; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-288309/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-OCT-1997;
                                                                                                                                       23-OCT-1997;
                                                                                                                (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                              cherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFLXXLRHSSLXRXCIXXICDFXXAFXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                          mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-00955636
                                                                                                                                         97US-00955636
                                                                                                                                                                98WO-US022152
                                                                                                                                                                                                                                    /note=
acid"
                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.9%;
97.7%;
                                                                                                                                                                                                                                              "Xaa= gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 172; DB 2;
Pred. No. 7.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                              acid, or glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Claim 7; Page 78; 86pp; English

Vitamin K-dependent polypeptide with modified of domain, useful for treating clotting disorders

gamma-carboxyglutamic

WPI; 1999-288309/24.

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RESULT 11
AAY18303
ID AAY18
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Best Local
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Query Match
Best Local S
Matches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein C
                                                                                       This sequence is the protein C GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as
                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY18303 standard; peptide;
                                                                                                                                                                                                                          Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic domain, useful for treating clotting disorders.
                                                                                                                                                                                                                                                                                                                                                23-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                         20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9920767-A1
                                                                                                                                                                                                Disclosure; Page 14; 86pp; English.
                                                                                                                                                                                                                                                                                                                     (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain; vitamin K-dependent protein; clotting disorder; therapy.
                                                                                                                                                                                                                                                                    1999-288309/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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  . Similarity
42; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANSFLXXLRQSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                ťo
                                                      44
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                                                                                the native
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           98WO-US022152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 .44
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.9%;
97.7%;
               95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Xaa=
                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172; DB 2;
Pred. No. 7.6e-21;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma-carboxyglutamic
  Score 172; DB 2;
Pred. No. 7.6e-21;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 44;
                              Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid,
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                                                                                                                                                                                                                                               acid
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Conservative

2.

0

Gaps

0;

RXS

ADD50094

RESULT 13 ADD50094

ADD50094 standard;

protein;

44

Å

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RESULT 12
AAB36402
ID AAB36
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                           Ś
                                                                      Query Match
Best Local 9
                                                            Matches
                                                                                                                                              affinity and the activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide and inhibits clot formation. (I) can have thrombolytic and haemostatic activities, and can be used as an inhibitor of clot formation. (I) is useful for decreasing clot formation in a mammal, a factor VII or factor IX containing a modified GLA domain is useful for increasing clot formation and for treating a bleeding disorder, including thrombosis and clotting disorders such as haemophilia B and liver disease. The present sequence represents a human protein C GLA domain sequence, given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gamma-carpoxygiutamic acid domain; factor IX; protein S; protein Z; factor X; prothrombin; enhanced membrane binding affinity; clot formation; thrombolytic; haemostatic; bleeding disorder; thrombosis; clotting disorder; haemophilia A; haemophilia B; liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitamin K-dependent protein; gamma-carboxyglutamic acid do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB36402 standard;
                                                                                                                                                                                                                                                                                                                                                                                         Novel vitamin K-dependent polypeptide useful for treating clotting disorders such as thrombosis and hemophilia, comprises modified gammacarboxy glutamic acid domain that enhances membrane binding affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB36402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2001
                                                                                                                                                                                                                                                                                                The present invention describes a vitamin K-dependent polypeptide comprising a modified gamma-carboxy glutamic acid (GLA) domain have least one amino acid substitution, that enhances membrane binding least one amino acid substitution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nelsestuen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 APR-2000; 2000WO-US011416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200066753-A2
                                                                                                                    Sequence 44
                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 42; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-007226/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-APR-1999;
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                              Н
                                                           l Similarity
42; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH
                            ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH
                                                                                                                        AA,
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C gamma-carboxyglutamic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-00302239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                           95.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44
                                                              Score 172; DB
Pred. No. 7.6e
2; Mismatches
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omain; factor IX; prote
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                                                                           DB 4;
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                                                                                           Length 44;
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Misc-difference Misc-difference

/note=

/note= "Gamma carboxylglutamic acid"

Location/Qualifiers

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RESULT 14
AAW75
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a vitamin K-dependent polypeptide comprising a modified gamma-carboxyglutamic acid (GLA) domain that enhances membrane binding affinity and activity of the polypeptide relative to a corresponding native vitamin K-dependent polypeptide, where the modified GLA domain comprises a glutamic acid residue at position 34. The polypeptide is useful in modulating clot formation in mammals or in treating certain types of haemophilia or clotting disorders. The membrane binding affinity of polypeptides is increased by site directed mutagenesis in the GLA domain. This sequence represents a vitamin K-dependent protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vitamin K-dependent polypeptide for modulating clot formation in mammals comprises a modified gamma-carboxyglutamic acid domain that enhances membrane binding affinity and activity of the polypeptide.
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29-APR-1999; 99US-00302239.
03-FEB-2000; 2000US-00497591.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2004 (first entry)
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                                                                                                 Gamma carboxylglutamic acid; human protein C; Gla domain; chimera; pRc/RSV; RSV-PC; amplification, PCR, primer; transfection; anticoagulant; human 293 cell; Protein S; myocardial infarction; venous thrombosis; disseminated intravascular coagulation; thromboembolic disease; lupus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-NOV-2002; 2002US-00298330.
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                                                                                                                                                                                                                                                                                                                                                                                                    AAW75710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW75710 standard; protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 1; 51pp; English.
                                                             adult respiratory distress syndrome; factor
                                                                                                                                                                                                                                                                     Partial human protein C amino acid sequence.
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                                                                 V Leiden; stroke
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                                                         Matches
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                                                                                                                                                   protein C protein, which contains gamma carboxylglutamic acid modified residues. This sequence was replaced with the corresponding regions of modified human prothrombin (AAW7509), to create a protein C protein C cDNA was ligated into procRsV to form RSV-PC, and then was digested with restriction enzymes to remove the first three exons and the first codon of exon four. The prothrombin cDNA was amplified, digested, and then 11st construct was then removed. This construct was then transfected into Numan 293 cells, from which the chimeric protein can be used as anticoagulant, to treat discrete where protein, site low, some forms of lugus, following stroke or myocardial infarction, after venous thrombosis and in disseminated intravascular coagulation, adult respiratory distress syndrome, in thromboembolic disease or factor venice.
                                                                                                                                                                                                                                                                                                                                                                                                                        Protein C chimeric proteins for use as anticoagulants - having gamma carboxyglutamic acid region replaced with Vitamin K dependent clotting factor e.g. prothrombin.
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Misc-difference 25
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                                                                                                               Sequence 45 AA;
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25-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                    The present sequence represents the first three exons of the human protein C protein, which contains gamma carboxylglutamic acid modified
                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OKLA-) OKLAHOMA MEDICAL RES FOUND.
                 1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                         42;
                                                                     Similarity
ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFQNVDDTLAFWSKH
                                                         Conservative
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97US-0053768P
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16
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                                                                    95.5%;
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                                                       Score 172; DB 2;
Pred. No. 7.8e-21;
2; Mismatches 0
                                                                                  Length 45;
                                                         Indels
   44
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ABB79947 standard; protein; 45 AA

Human protein C Gla domain. 12-DEC-2002 (first entry) ABB79947;

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                                                                                                                                                                           The present sequence is the protein sequence of the Gla domain (N-CC terminal amino acids 1-45) of human protein C. The invention provides CC human protein C and activated protein C variants in which the Gla domain C contains at least 6, and optionally 7-10, amino acid substitutions, CC preferably the substitution mutations H100, S11G, S12N, D23S, D32B, N33D CC and H44Y (see ABB79946). Protein C variants comprising the mutated Gla CC clotting time in standard in vitro coagulant activity, as shown in increased CC clotting time in standard in vitro coagulation assays, as a result of CC enhanced calcium and/or membrane binding properties. The invention CC provides methods for producing the variants based on DNA technology, and CC for using the variants in the treatment of coagulation disorders such as CC thrombosis or APC resistance, or in diagnostic test systems for assaying CC components of the protein C-anticoagulant system (all claimed). The CC variants may also be used in treating arteriosclerosis, myocardial CC infarction, and disseminated intravascular coagulation
                                                                         Matches
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New variant blood coagulation component, useful for manufacturing a medicament for treating or preventing coagulation disorders, e.g. thrombosis, comprises an anticoagulant activity in the protein C-anticoagulant system of blood.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein C; Gla domain; human; blood clotting; anticoagulant; thrombolytic; antiarteriosclerotic; cardiant; antiaggregant.
                                                                                                                                              Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 7; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-713449/77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dahlbaeck B;
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                                                                     Score 172; DB 5; Length 45; Pred. No. 7.8e-21; Mismatches 9; Indels
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Search completed: March Job time : 52 secs

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Compugen Ltd.
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				- numan protein C 987 #text 0927 r human p: r 2991887
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-		ม	RESULT 1	procent c (actuates) (EC 3.4.21.09) precursor - numan N.Alternate names autoprothrombin IIA; plasma protein C.Species: Homo sapiens (man) C.Sate: 17-Mar-1987 #sequence revision 17-Mar-1987 #tex C.Accession: A22331; A25426; A2181; A23789; A00927 C.Accession: A22331; A25426; A2181; A23789; A00927 R.Poster, D.C.; Yoshitake, S.; Davie, E.W. Proc. Natl. Acad. Sci. U.S. A. 82, 4673-4677, 1985 A.Title: The nucleotide sequence of the gene for human A.Reference number: A22331; MUID:85270390; PMID:2991887 A.Molecule type: DNA
			成 数 (42 OOO E A A A A A

A; Residues: 1.451. PROSINGE BM MILES BY NID G190133; PIDN: AAA60166.1; PID: G190334

R; PIULEZKY, U.; ROSKINS, U.S., Long, G.L.; Crabtree, G.R.

R; PIULEZKY, U.; ROSKINS, U.S., Long, G.L.; Crabtree, G.R.

A; Reference number: A25426; MUID: 86120978; PMID: 3511471

A; Accession: A25426

A; Molecule type: DRA

A; Residues: 1.445, L', 446-461 PLU>

A; Residues: G:RM1212; NID: 9190330; PIDN: AAA60165.1; PID: 9190332

B; Roster, D.; Davie, E.M.
A; Residues: G:RM1212; NID: 9190330; PIDN: AAA60165.1; PID: 9190332

B; Roster, D.; Davie, E.M.
A; Residues: G:RM20269; NID: 9190322; PIDN: AAA60164.1; PID: 9190332

A; Residues: G:RM20269; NID: 9190322; PIDN: AAA60164.1; PID: 9190332

A; Residues: G:RM20269; NID: 9190322; PIDN: AAA60164.1; PID: 9190323

A; Residues: G:V. 107-461 PROSIDE A37714; PMID: 6599623

A; Residues: G:RM20269; NID: 9190322; PIDN: AAA60164.1; PID: 9190323

A; Residues: G:RM20269; NID: 9190322; PIDN: AAA60164.1; PID: 9190323

A; Residues: G:RM20269; NID: 9190322; PIDN: AAA60164.1; PID: 9190323

A; Residues: G:RM20269; NID: 9190323; PIDN: AAA60164.1; PID: 9190323

A; Residues: G:RM20269; NID: 9190323; PIDN: 9190323

A; Residues: G:RM20269; MUID: 9190329; PMID: 2991859

A; Residues: A27389; MUID: 9190899; PMID: 2991859

A; Residues: A27389; MUID: 9190899; PMID: 2991894; PMID: 644179

A; Residues: G:RM20269; MUID: 91908999; PMID: 91908999; PMID: 91909999

A; Title: Deta protein C is not G; Procession: A2739; and the beta form is not A; Title: Deta protein C is g19cosylated at Asn-329, and the beta form is not A; Title: OHM: A4605; MUID: 91909104; PMID: 9184894

A; Reference number: A4605; MUID: 9190910404; PMID: 9184894

A; Reference number: A4605; MUID: 9190999999; PMID: 9184894

A; Reference number: A4605; MUID: 91

plasma protein S p plasma protein Z -plasma protein Z p probable MAP kinas

hrombin (EC 3.4.2 coagulation factor

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A;Urbors: 24/1; 79/3: 881.; 134/1; 179/1; 256/3; 266/1
A;Introns: 24/1; 79/3: 881.; 134/1; 179/1; 256/3; 266/1
C;Superfamily: coagulation factor X: EGF homology; Gla domain homology;
C;Superfamily: coagulation factor X: EGF homology; Gla domain homology;
C;Superfamily: coagulation factor X: EGF homology; Gla>
C;Superfamily: coagulation factor X: EGF homology Gla>
C;Superfamily: Signal sequence #status predicted <SIG>
F;27-86/Domain: Signal sequence #status predicted <LGH>
F;27-86/Domain: propeptide #status predicted <LGH>
F;33-42/Domain: EGF homology GGG>
F;92-131/Domain: EGF homology GGG>
F;92-131/Domain: EGF homology GGG>
F;200-46/PFroduct: protein C leavy chain #status predicted <HCH>
F;200-46/PFroduct: protein C feavy chain #status predicted <HCH>
F;200-211/Domain: trypsin homology GGG>
F;212-445/Domain: trypsin homology GTR>
F;212-445/Domain: trypsin homology GTR>
F;200-211/Domain: trypsin homology GTR>
F;210-45/Domain: trypsin homology GTR>
F;210-46/PFroduct: protein C factor Gamma-carboxyglutamic acid (Glu) #status exprimental
F;211-10Finding site: carbohydrate (AFN) (covalent) #status absent
F;110/Finding site: carbohydrate (AFN) (covalent) #status experimental
F;213-290,355/Binding site: carbohydrate (AFN) (covalent) #status experimental
F;253,299,402/Active site: His, Asp, Ser #status predicted
F;371/Binding site: carbohydrate (AFN) (covalent) (partial) #status atypical
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F;24-85/Domain: domain homology <GLA.
F;34-41/Domain: propeptide #status predicted <PRC>
F;42-196,199-461/Product: protein C #status predicted <PRC>
F;42-196/Domain: BGF homology <EG2>
F;139-174/Domain: BGF homology <EG2>
F;139-174/Domain: BGF homology <EG2>
F;139-174/Domain: activation peptide #status predicted <PCH>
F;139-174/Domain: activation peptide #status predicted <ACT>
F;131-146/Domain: activation peptide #status predicted <ACT>
F;131-146/Domain: activation peptide #status gamma-carboxyglutamic acid (Glu) #status F;112/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted F;112/Modified site: carbohydrate (Asn) (covalent) #status predicted F;214,230,355/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;253,299,402/Active site: His, Asp, Ser #status predicted
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A,Residues: 1-461 <TAD>
A,Residues: 1-461 <TAD>
A,Experimental source: 11ver
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C;Genetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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NA-lerander names: vitamin K-dependent serine proteinase
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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R;Tada, N.; Sato, M.; Tsujimura, A.; Iwase, R.; Hashimoto-Gotoh, T.
Biochhem. 111, 491-495, 1992
A;Title: Isolation and characterization of a mouse protein C cDNA.
A;Reference number: JX0210; MUID:92316897; PMID:1618739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.9%; Score 172; DB 1; Length 461;
75.0%; Pred. No. 1e-19;
.ive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 ANSFLEEDRHSSLERECIERICDFERAKEIFONVDDTLAFWSKH 86
                                                                                                                                                                                                                                         A; Cross-references: GDB:120317; OMIM:176860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 75.0
Matches 33; Conservative
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A,Molecule type: mRNA
A,Residues: 1-461 <OKA2>
A,Residues: 1-461 <OKA2>
A,Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
C,Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C,Keywords: beta-hydroxyaspartic acid; glycoprotein; hydrolase; serine proteinase
F;1-32/Domain: signal sequence #status predicted <SIG>
                                                           ô
                                                                                                                                                                                                                                                                                                                               protein C (activated) (EC 3.4.21.69) precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Dacession: 518994; S24312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
submitted to the RMBL Data Library, Rebruary 1992
A;Description: The CDNA clonining and mRNA expression of rat protein C.
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N;Alternate names: autoprothrombin IIA; plasma protein C
S;Species: Bos prindgenius taurus (cattle)
C;Date: 30-Nov-1980 #sequence revision 17-Mar-1987 #text_change 16-Jul-1999
C;Accession: A26250; A18385; A18386; A00928
R;Long, G.L.; Balaqaje, R.M.; MacGilliuvray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 81, 5631-5656, 1984
A;Title: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963 R;Okathi, T.; Makawa, K.; Nawa, K.; Matumoto, Y. Biochim. Biochim. Biochim. Biochim. 329-332, 1992 A;Title: The cDNA cloning and mRNA expression of rat protein C. A;Reference number: S24312; MOID:92329550; PMID:1627650 A;Status: preliminary
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67.2%; Score 133; DB 1; Length 461; 56.8%; Pred. No. 2e-13; Live 7; Mismatches 12; Indels
                                                                                                                    1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                42 ANSFLEEMRPGSLERECMBEICDFEEAQBIFONVEDTLAFWIKY 85
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                             Local Similarity 56.8
es 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Molecule type: mRNA
A,Residues: 1-456 <LON>
R,Fernlund, P.; Stenflo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-461 < OKA>
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A;Status: preliminary
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      Query Match
                                    Best Loca
Matches
                                                                                                                                                                                                                                                                             RESULT 3
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Gaps

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A; Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre A; Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pre A; Description: cagulation factor X; EGF homology; Gla domain homology; trypsin homology C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami; C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutami; F; 1-23/Domain: EGF homology cagla.

F; 25-84/Domain: EGF homology cagla.
F; 26-121/Domain: EGF homology cagla.
F; 129-164/Domain: EGF homology cagla.
F; 139-140/Domain: EGF homology cagla.
F; 139-210/Domain: EGF homology cagla.
F; 139-231/Domain: EGF homology cagla.
F; 139-231/Domain: activation factor X heavy chain #status predicted cagla.
F; 232-482/Product: coagulation factor X heavy chain #status predicted cagla.
F; 232-482/Product: coagulation factor X heavy chain #status predicted cagla.
F; 232-460/Domain: trypsin homology cagra.
F; 232-460/Domain: trypsin homology cagra.
F; 240,123-462,361.11,112-112,129-140,138-149,151-164,172-340,238-243,259-275,388-402,413.
F; 103/Modified site: erychro-beta-hydroxyasparic acid (Asp) #status predicted
F; 108/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 218/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 217,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-141,132-1
                                                                                                                                                                                                                                                                     complete translation are shown
                                                      A; Molecule type: mRNA
A; Residues: 1-482 < CTN1>
A; Residues: 1-482 < CTN1>
A; Note: references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A; Note: submitted to the EMBL Data Library, June 1994
A; Note: neither the complete nucleic acid sequence nor the complete translation are s: R; Stanton, C:; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A; Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A; Reference number: JC4670; MUID:96194815; PMID:8647460
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A;Residues: 183-186,'X',188-207 <ENJ2>
A;Residues: 183-186,'X', 188-207 <ENJ2>
R;Murzakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.
Eur. J. Haematol. 52, 162-168, 1994
A;Title: Analysis of the partial nucleotide sequences and deduced primary structures
A;Reference number: 146196; MUID:94222160; PMID:8168596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1482 <CTA2.
A; Residues: 1482 <CTA2.
A; Cross-teferences: EMBL: X79807; NID: 9506600; PIDN: CAA56202.1; PID: 9506601
A; Experimental source: Cos-1 cell
B; Emjyoji, K.; Miyazaki, K.; Kato, H.
J. Biochem: 109, 890-898, 1991
A; Title: Characterization of rat factors X and Xa: demonstration of factor Xa A; Reference number: PS0190; MUID: 92041742; PMID: 1718949
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NiAlternate names: Stuart factor
C.Species: Bos primigenius faurus (cattle)
C.Species: 44-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA_
A;Residues: 295-383,'G',385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
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Pred. No. 3.3e-09;
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A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Residues: 41-58,'X',60-65 <ENJ1>
A,Accession: PS0190
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Best Local Similarity 40.9
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: JC4670
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A; Residues: 197-454, PV' - GSTE>
B; Resman, N.L.; Dasult, L.E.; Esmon, C.T.
J. Biol. Chem. 258, 5548-5553, 1983
A; Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless pareference number: A37541; MUID: 821513; PMID: 6304092
A; Contents: annotation; activation; calcium binding
A; Contents: annotation; Late, T.M.; Esmon, C.T.
J. Biol. Chem. 258, 5554-5560, 1983
A; Title: Structural changes required for activation of protein C are induced by Ca2+ bin A; Reference number: A37542; MUID: 83213514; PMID: 6406503
A; Contents: annotation; activation; calcium binding
C; Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reactif
C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strc
cognition of the thrombin-thrombomodulin complex.
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keyworts. signal sequence (fragment) #status predicted cSIG>
F;14-83/Domain: signal sequence (fragment) #status predicted cSIG>
F;40-194/Promain: Dropeptide #status predicted cPRO>
F;80-128/Domain: EGF homology cEGI>
F;3137-127.Domain: EGF homology cEGI>
F;3137-127.Domain: EGF homology cEGI>
F;3137-127.Domain: EGF homology cEGI>
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Fig7-456/Product: protein C heavy chain #status experimental <APT>
Fig97-210/Domain: artivation peptide #status experimental <APT>
Fig11-40/Domain: trypsin homology <ART  
Fig110-40/Domain: trypsin homology <ART  
Fig110-455,58,58,59,62,64,65,68,74/Modified site: gamma-carboxyglutamic acid (Glu) #stat  
Fig110-458,33,55,58,59,59,59,59,74,759-172,180-318,237-253,368-382,393-421/Disulfide bonds: #stat  
Fig110-458,350/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;252,298,397/Active site: His, Asp, Ser #status predicted  
F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Jan-1995 #sequence_revision 07-Feb-1997 #text_change 08-Dec-2000
C.Accession: 849075; JC4670; FS0191; PS0190; I62745
R.Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
A.Fromb. Res. 80, 63-73, 1995
A.Friel: Evidence for competition between vitamin K-dependent clotting factors for intra
A.Reference number: A58498; MUID:96093366; PMID:8578539
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J. Biol. Chem. 257, 12170-12179, 1982
A;Title: Amino acid sequence of the light chain of bovine protein
A;Reference number: A18385, MUID:83007325, PMID:6896876
                                                                                                                                                                                                                                                                                                A)Note: 82-193 was also found

R)Drakenberg, T.; Fernlund, P.; Roepstorff, P.; Stenflo, J.

Brod. Natl Acad Sci. U.S.A. 80, 1802-1806, 1983

A)Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein

A)Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein

A)Reference number: A19316; MUID:83169769; PMID:6572939

A)Contents: annotation; revision to residue 110

R;Stenflo, J; Pernlund, P.

Biol. Chem. 257, 12180-12190, 1982

A)Title: Amino acid sequence of the heavy chain of bovine protein

A)Reference number: A18386; MUID:83007326; PMID:6896877
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Best Local Similarity 47.6%; Pred. No. 1.6e-10;
Matches 20; Conservative 9; Mismatches 13; Indels
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                                                                                                                                                                                                                    A, Molecule type: protein
A, Residues: 40-194 < FER>
                                                                                                                                                             ;Accession: A18385
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Accession: A22867

Accession: A14997

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A, Describtion: catalyzes the proteclytic activation of prothrombin to thrombin in the properties degretation factor X; EGF homology; Gla domain homology of Steperfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology; C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam: F;1-1s/Domain: signal sequence #status predicted <PRO> F;25-84/Domain: gla domain homology cGib. F;25-84/Domain: EGF homology cGib. F;25-84/Domain: EGF homology cGib. F;29-164/Domain: EGF homology cEG2> F;129-164/Domain: EGF homology cEG2> F;129-164/Domain: EGF homology cEG2> F;129-164/Domain: EGF homology cEG2> F;183-492/Product: coagulation factor X heavy chain #status experimental cAHC> F;29-164/Domain: activation peptide #status experimental cAHC> F;29-164/Domain: activation factor X heavy chain #status experimental cAHC> F;24-461/Domain: activation factor X heavy chain #status experimental cAHC> F;24-461/Domain: activation peptide #status experimental cativation factor in the properties of the properties 
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: Az4478; JG0917; Az485; Az5853; Az2208; Az1284; Az0362; S39415; I54051; A00°
C;Accession: Az4478; JG0917; Az485; Az5853; Az2208; Az1284; Az0362; S39415; I54051; A00°
R;Leytus, S.P.; Foster, D.C.; Kurachi, K.; Davie, E.W.
Biochemistry 25, 5098-5102, 1986
Biochemistry 25, 5098-5102, 1986
A;Attle: Gene for human Factor X: a blood coagulation factor whose gene organization is & A;Accession: Az4478; MUID:87026600; PMID:3768336
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A,Residues: 1-488 <LEEY.
A,FCROSS-references: GB:L29433; GB:M14327; NID:g458809; PIDN:AAA52764.1; PID:g182831
R,Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
B,Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
A,Fittle: Cloning and expression in COS-1 cells of a full-length cDNA encoding human coagn
A,Reference number: JQ0917; MJID:91216473; PMID:1902434
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R;Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
J. Biol. Chem. 267, 7395-7401, 1992
A;Title: Liver-specific expression of the gene coding for human factor X, a blood coagula A;Reference number: A42485; MUID:92218390; PMID:1313796
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R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
Gene 41, 311-314, 1886
A;Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A;Reference number: A25853; MUID:86221713; PMID:3011603
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A;Residues: 1-15 <MIA>
A;Experimental source: liver
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A;Residues: 1-488 <MES>
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A,Reference control of the control of dectivated Stuart factor). Evidence of homology with mammali A,Reference number: A1243; MUID:3053314; PMID:4264286
A,Contents: annotation; active site
R,Rulikawa, K, Titani, K, Jadvie, E.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A,Title: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to A,Reference number: A13504; MUID:76053121; PMID:1059122
A,Contents: annotation; activation
B,Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J, Biol. Chem. 259, 5705-5710, 1984
A,Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic A,Reference number: A38024; MUID:84185716; PMID:3546930
A,Contents: annotation; calcium binding
R;Morita, T.; Jackson, C.M.
J, Biol. Chem. 261, 4008-4014, 1986
A,Reference number: A38025; MUID:86140110; PMID:3949800
A,Contents: annotation; sulfate binding
C,Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C,Comment: Ractor Xa converts prothrombin to thrombin during blood clotting.
C,Comment: The two chains are formed from a single-chain precursor by the excision of tw C,Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: beta-hydroxyaspartic acid site
Inoue, K.; Morita, T.
ur. J. Biochem. 218, 153-163, 1993
Yitle: Identification of O-linked oligosaccharide chains in the activation peptides of
Reference number: S39414; MUID:94062825; PMID:8243461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strd
C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
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A; Meddues: 183-292, 294-295, GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <7
A; Nesaidues: 183-292, 294-295, 'GDE', 299-334, 336-348, 'AE', 351-354, 356-441, 'GKFG', 446-492 <7
A; Note: carbohydrate binding sites and disulfide bonds were determined
B; Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
C, Balo, Chem. 264, 1889-18994, 1889
A; Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
A; Reference number: A34412; MUID:89380326; PMID:2789221
C;Accession: A22867; A14997; A12030; A34412; S39414; A00925
R;Fung, M.R.; Campbell, R.M.; MacGillivray, T.A.
Nucleic Acids Res. 12, 4481-4492, 1984
A;Title: Blood coagulation factor X mRNA encodes a single polypeptide chain containing A;Reference number: A22867; MUID:84247315; PMID:6330671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecule type: protein
,Residues: 41-102, W. / 104-180 < ENF>
,Residues: 41-102, W. / 104-180 < ENF>
,Residues: 41-102, W. / 104-180 < ENF>
,Modwillen, B.A.; Eujikawa, K.; Kisiel, W.
iochem. Biophys. Res. Commun. 115, 8-14, 1983
,/Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood c. Reference number: A20274; MUID:83308813; PMID:6688526
,/Tontents: annotation; revision to residue 103
,/Tontents: annotation; revision to residue 103
,/Titleni, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
roc. Natl. Acad. Sci. U.S.A. 72, 3082-3086, 1975
,/Title: Bovine factor X.1 (Stuart factor): amino-acid sequence of heavy chain.
,Reference number: A12030; MUID:76053069; PMID:1059093
                                                                                                                                                                                                                                                                                                                                                                                                               ; Molecule type: mRNA; ROMS.
; Residudes: 1.487 - (PUN) - (ROMS); ROMS - (ROMS);
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A;Accession: A34412 A;Molecule type: protein A;Residues: 85-126 <PER>

A,Gene: F10 A,Map position: 13q34

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coagulation factor VII - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Accession: 146932

R;Brothers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.

Thromb. Res. 69, 231-238, 1993

A;Title: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.

A;Reference number: 146932; MUID:93190306; PMID:8383365

A;Reference number: 146932; MUID:93190306; PMID:8383365

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Status: preliminary;
A;Molecule type: mRNA

A;Residues: 1-443 «BRO»

A;Cross-references: GB:856300; NID:9266295

C;Superfamily: coagulation factor X; EGF homology; Gla domain homology cEGL»

F;89-120/Domain: EGF homology <EGL»

F;130-126/Domain: EGF homology <EGL»

F;130-166/Domain: EGF homology <EGL»

F;130-166/Domain: trypsin homology <ERS»
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C;Species: Homo sapiens (man)
C;Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000 |
C;Date: 19-May-1989 #sequence revision 19-May-1994 #text_change 08-Dec-2000 |
C;Accession: A28322; A23819; A31186; B31186; S63524 #text_change 08-Dec-2000 |
R;O'Hara, P.J': Grant, F.J.; Haldeman, B.A.; Gray, C.L.; Insley, M.Y.; Hagen, F.S.; Wurr: Proc. Natl. Acad. Sci. U.S.A. 84, 5158-5162, 1987
A;Title: Nucleotide sequence of the gene coding for human factor VII, a vitamin K-depends A;Reference number: A28322; MUID:87260948; PMID:3037537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-466 < HAG>
A; Residues: 1-466 < HAG>
A; Cross-references: GB:M13232; NID:g182799; PIDN:AAA88040.1; PID:g182801
R; Thim. L.; Bjoern, S.; Christensen, M.; Nicolaisen, E.M.; Lund-Hansen, T.; Pedersen, A.}
Biochemistry 27, 7785-7793, 1988
A; Title: Amino acid sequence and posttranslational modifications of human factor VII-a fi
A; Reference number: A90539; MUID:89088153; PMID:3264725
A; Accession: A1186
A; Molecule type: protein
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental F;211,211/Binding site: carbohydrate (Asn) (covalent) #status experimental F;231,231/Binding site: carbohydrate (Asn) (covalent) #status experimental F;234,235/Cleavage site: Arg-1le (coagulation factor IXa, coagulation factor VIIa) #statu F;275,322,419/Active site: His, Asp, Ser #status experimental
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A,Cross-references: GB:002933; NID:g180333; PIDN:AAA51983.1; PID:g180334
R;Hagen, F.S.; Gray, C.L.; O'Hara, P.; Grant, F.J.; Saari, G.C.; Woodbury, R.G.; Hart, C
Proc. Natl. Acad. Sci. U.S.A. 83, 2412-2416, 1986
A;Title: Characterization of a cDNA coding for human factor VII.
A;Reference number: A23819; MUID:86205965; PMID:3486420
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                                                                                                                                                                                                                                                                                                         Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                         18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKY 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 ANSFLEELRPGSLERECKEELCSFEEAREVFOSTERTKOFW 80
                                                                                                                                                                                                                                                                                                    51.5%; Score 102; DB 1;
40.9%; Pred. No. 2.1e-08;
tive 8; Mismatches 18;
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Best Local Similarity 43.9%
Matches 18, Conservative
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Matches 18; Conservative
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A; Residues: 1-466 <OHA>
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Fi139-486/Product: coaquitation factor X heavy chain #status experimental <HCH>
Fi139-486/Product: coaquitation factor Xa heavy chain #status experimental <APT>
Fi135-486/Product: coaquiation factor Xa heavy chain #status experimental <ACT>
Fi235-465/Domain: trypsin homology <TRY>
Fi355-465/Domain: trypsin homology <TRY>
Fi46.47,54,56,59,60,65,66,69,72,79/Modified site: gamma-carboxyglutamic acid (Glu) #station file bonds: #status predicted
Fi57-62/Disulfide bonds: #status predicted
Fi57-62/Disulfide bonds: #status predicted
Fi590-101,95-110,112-121,129-140,136-149,151-164,172-342,241-246,261-277,390-404,415-443)
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A; Residuce: 13.284, EV. 289-488 < LE2>
A; Residuce: 13.284, EV. 289-488 < LE2>
A; Cross-references: GB: K01886
R; McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weine
Biochemistry 22, 2875-2884, 1983
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C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam
F; 1-23/Domain: signal sequence #status predicted <SIG>
F; 24-40/Domain: propeptide #status predicted <PRO>
F; 25-84/Domain: Gla domain homology <GLA>
F; 21-179/Product: coagulation factor X light chain #status experimental <LCH>
F; 90-121/Domain: EGF homology <EGI>
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ur. J. Biochem. 218, 153-163, 1993
yr. J. Biochem. 218, 153-163, 1993
yritle: Identification of O-linked oligosaccharide chains in the activation peptides of Reference number: 839414; MUID:94062825; PMID:8243461
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A; Contents: annotation; X-ray crystallography, 2.2 angstroms
Comment: The two chains held together by one disulfide bond are formed from a single-of C; Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) or
                                          7; Fung, M.R.; Hay, C.W.; Macgillivray, R.T.A.
Proc. Matl. Acad. Sci. U.S.A. 82, 3531-3555, 1885
3; Title: Characterization of an almost full-length colla coding for human blood coagulati
3; Reference number: A22208; MUID:85216545; PMID:2582420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title: Complete amino acid sequence of the light chain of human blood coagulation fact; Reference number: A20362; MUID:83257207; PMID:6871167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: glycosylation sites A;Note: dentification of beta-hydroxyaspartic acid A;Note: ddentification and characterization of beta-hydroxyaspartic acid R;Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G. Gene 84, 517-519, 1989
A;Title: Clonining and characterization of the 5' end (exon 1) of the gene encoding human A;Reference number: 154051; MUID:90128299; PMID:2612918
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R;Paddmanabhan, K.; Paddmanabhan, K.P.; TulinsKy, A.; Park, C.H.; Bode, W.; Huber, R.; Bla
J. Mol. Biol. 232, 947-966, 1993
A;Title: Structure of human des(1-45) factor Xa at 2.2 angstroms resolution.
                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residuae: 13-441, S',443-488 <FUN>
A; Residuae: 13-441, S',443-488 <FUN>
A; Cross references: GB: R03194; NID:9182840; PIDN:AAA52490, 1; PID:9182841
R; Leytus; S.P.; Chung, D.W.; Kisiel, W.; Kurachi, K.; Davie, E.W.
Proc. NALL, Acad. Sci. U.S.A. 81, 3699-3702, 1984
A; Title: Characterization of a cDNA coding for human factor X.
A; Reference number: A21284; MUID:84222026; PMID:6587384
     A;Cross-references: GB:M22613; NID:g180335; PIDN:AAA51984,1; PID:g180336
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A;Map position: 13q34-13q34
A;Introns: 244/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1
A;Note: deficiency of this factor causes Stuart disease
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A;Residues: 183-234 <INO>
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A; Residues: 1-23 < RES>
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seq1-32glu-33asp.rpr

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39.6%; Score 78.5; DB 2; Length 618;
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Matches 1
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Persson, B.; Petersen, L.C.
ur. J. Blochem. 234, 299-300, 1995
ur. J. Blochem. 234, 299-300, 1995
fittle: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox;Reference number: 863524; MUID:96096752; PMID:8529655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;213-447/Domain: trypsin homology <TRX>
F;66,67,74,76,79,80,85,86,89,95/Wodified site: gamma-carboxyglutamic acid (Glu) #status
F;66,67,74,76,79,80,85,86,89,95/Wodified site: gamma-carboxyglutamic acid (Glu) #status
F;712,120,110-1121,115-130,132-141,151-162,158-172,174-181,95-219-224,238-254,370-389,
F;112,120,20,80,80,81c: carbohydrate (Ser) (covalent) #status experimental
F;205,382/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;212-213/Cleavage site: Arg-IIe (coagulation factor XIa) #status experimental
F;253,302,404/Active site: His, Asp, Ser #status predicted
F;350-351/Cleavage site: Arg-Gly (coagulation factor Xa) #status predicted
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C;Accession: S10511; A60576; E42696
R;Dihanich, M.; Monard, D.
Nucleic Acids Res. 18, 4251, 1990
A;Title: oDNA sequence of rat prothrombin.
A;Reference number: S10511; MUID:90332426; PMID:2377469
A;Reference number: S10511; MUID:90332426; PMID:2377469
A;Reference number: BMB:X52835; NID:g56969; PIDN:CAA37017.1; PID:g56970
A;Reinius type: mRNA
A;Residus: 1-67: A32in, B.E.; Greenwood, J.A.; Dickerman, H.W.
B:Henrikson, K.P.; Jazin, B.E.; Greenwood, J.A.; Dickerman, H.W.
A;Cross-reference number: A60576; MUID:90091942; PMID:2293980
A;Reference number: A60576
A;Molecule type: protein
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A;Map position: 13q34-13q34
A;Introns: 22/1; 44/1; 97/3; 106/1; 144/1; 191/1; 227/3; 269/1
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                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
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46.3%; Pred. No. 8.3e-07;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                     Accession: S63524
                                                                                                                                                                                                                                                                                                                                                                                                         Gene: GDB:F7
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A,Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute:
R,Banfield, D.K.: MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A,Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seqn A,Reference number: A42696; MUID:92212913; PMID:1557383
A,Accession: B42696
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: Dreliminary
A,Molecule type: mRNA
A,Residues: 33.8-617, EV. GBNN>
A,Cross-references: GB:M81397
C,Superfamily: thrombin; Gla domain homology, kringle homology; trypsin homology
C,Reywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydr:
F;1-24/Domain: spropeptide #status predicted <PRO>
F;28-88/Domain: gla domain homology <GLA>
F;461/Promain: propeptide #status experimental <PNAT>
F;461-104/Domain: kringle homology <KR2>
F;26-604/Domain: kringle homology <KR2>
F;26-604/Domain: kringle homology <KR2>
F;26-604/Domain: kringle homology <KR2>
F;26-604/Domain: kringle homology <RR2>
F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5
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A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 384-618, E' < CAN>
A, Cross-references: GB:M81394
C. Superfamily: thrombin; Gla domain homology; kringle homology trypsin homology
C. Superfamily: thrombin; Gla domain predicted < SIG>
E, S-44 Domain: signal sequence #status predicted < FRO>
E, S-544 Domain: gropeptic de #status predicted < FRO>
E, S-64 Domain: kringle homology < CLA>
E, SIG-18, Product: prothrombin B #status predicted < MAT>
E, SIG-18, E, SIG-18, E, Molecule to MAT>
E, SIG-18, E, SIG-18, E, Molecule E, E, SIG-18, E, SIG-
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C;Species: Mus musculus (house mouse)
C;Date: 14-Dec-1990 #sequence revision 14-Dec-1990 #text_change 03-May-2002
C;Accession: A35827; A42696; S12081
R;Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.
DNA Cell Biol. 9, 487-498, 1990
A;Title: Characterization of the cDNA coding for mouse prothrombin and localization of th
A;Reference number: A35827; MUID:9102551; PMID:2222810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)Status: preliminary
A)Molecule type: mRNA
A,Molecule the data were obtained from females resulting from the cross of M. domesticus and
R,Banfield, D.K., MacGillivray, R.T.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A,Title: mattain characterization of vertebrate prothrombin cDNAs: amplification and sequence number: A42696, MUID:92212913; PMID:1557383
A,Accession: A42696
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A;Accession: A37549
A;Nolecule type: protein
A;Rosidues: 44-118,'N', 120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-308,'
A;Residues: 44-118,'N', 120,'S',122-163,'I',165-175,'A',177-182,'T',184-193,'MV',196-308,'
R;Butkowski, R.J.; Elion, J.; Downing, M.R.; Mann, K.G.
J. Biol. Chem. 225, 4942-4957, 1977
A;Title: Primary structure of human prethrombin 2 and alpha-thrombin.
A;Reference number: A37550; MUID:77207112; PMID:873923
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A; Residues: 315-334, N, 336-348, NV, 350-368, NV, 370-397, NV, 399-413, NV, 415-484, NV, 486-4
B; Residues: 315-334, NV, 336-348, NV, 350-368, NV, 370-397, NV, 399-413, NV, 415-484, NV, 486-4
B; Residues: 315-334, NV, 136-13215, 1986
A; Reference number: A37551; MUID: 87008532; PMID: 3759958
A; Contents: annotation; activation cleavages
B; MacGillivray, R.T.; Irwin, D.M.; Guinto, E.R.; Stone, J.C.
Ann. N. Y. Acad. Sci. 485, 73-79, 1986
A; Title: Recombinant genetic approaches to functional mapping of thrombin.
A; Reference number: 151952; MUID: 87182874; PMID: 3471151
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A/Status: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-2, RI', 5-100 cRES>
A/Residues: 1-2, RI', 5-100 cRES>
A/Cross-references: GB-MAJ001; NID:g190723; PIDN:AAA60220.1; PID:g190724
A/Cross-references: GB-MAJ001; NID:g190723; PIDN:AAA60220.1; PID:g190724
CCCmment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrit CCCmment: Thrombin; which cleaves bonds after Arg and Lys, converts fibrinogen to fibrit CCCmment: The cleaves after Arg and Lys, converts fibrinogen to fibrit CCCmment: The cleaves after Arg-198, observed in vitro, does not occur in plasma.
C/Comment: The gamma-carboxyglutamy residues bind calcium ions, result from the carboxyl cccmment: The prothrombin precursor is synthesized in the liver.
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A;Map position: 11p11-11q12
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplic
C;Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; duplic
F;1-44/Domain: signal sequence #status predicted <SIG>
F;2-44/Domain: propeptide #status predicted <PRO>
F;28-87/Domain: Gla domain homology <GIA>
F;44-622/Product: prothrombin #status experimental <AMT>
F;44-527/Product: prothrompin #status experimental <AMT>
F;44-327/Domain: activation peptide #status Experimental <AMT>
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F)218-291/Domain: kringle homology «KR2»
F)218-291/Domain: kringle homology «KR2»
F)38-363/Product: thrombin light chain #status experimental «HCH»
F)364-622/Product: thrombin heavy chain #status experimental «HCH»
F)364-613/Domain: trypsin homology «TRY»
F)364-613/Domain: trypsin homology «TRY»
F)364-65,90-103,108-186,129-169,157-181,213-291,234-274,262-286/Disulfide bonds: #status
F)360-65,90-103,108-186,129-169,157-181,213-291,34-274,262-286/Disulfide bonds: #status
                                                                                                                                                                                                                          A,Accession: A29351
A,Molecule type: DNA
A,Residues: 1-62-DEG>
A,Cross-references: GB:M17262, GB:M33691, NID:G558069; PIDN:AAC63054.1; PID:g339641
A,Cross-references: GB:M17262, GB:M33691, NID:G558069; PIDN:AAC63054.1; PID:g339641
B;Degon, S.J.F.; Macdillivray, R.T.A.; Davie, E.W.
Biochemistry 22, 2087-2097, 1983
A,Title: Characterization of the complementary deoxyribonucleic acid and gene coding
A,Reference number: A00914; MUID:83231469; PMID:6305407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A/Accession: A00914.

A/Molecule type: mRNA
A/Residues: 8-163, NV,165-622 <DE2>
A/Cross-references: GB:V00595; GB:J00307; NID:g37128; PIDN:CAA23842.1; PID:g1335344
A/Accession: B00914
A/Accession: B00914
A/Rolecule type: DNA
A/Residues: 188-311 <DE3>
A/Residues: 188-311 <DE3>
A/Residues: 188-311 <DE3>
A/Residues: A37549; MJD:77193964; PMID:266717
                 Ribegen, S.J.F.; Davie, E.W.
Biochemistry 26, 6165-6177, 1987
A:Title: Nuclectide sequence of the gene for human prothrombin.
A;Reference number: A29351; MUID:88077877; PMID:2825773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Receivation: 1999: protein
A; Receivation: 1999: protein
A; Receivation: 1990: crax.
B; Rechaulten, B.A.; Fujikawa, K.; Kisiel, W.
B; Rechaus: 1-40° crax.
B; Rechaus: 1-40° crax.
B; Rechaus: 1-40° crax.
B; Rechaulten, B.A.; Fujikawa, K.; Kisiel, W.
B; Rechaulten, B.A.; Fujikawa, K.; Fujikawa, K.; Risiel, W.
B; Rechaulten, B.A.; Fujikawa, K.; Resion: Corg.
A; Reference mumber: A20274, MUD183308813; PMID: 668826
B; Rissel, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, A; Risiel B; Beca, X.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, B; Rissel, S.; Kawabata, S.; Nishimura, H.; Takeya, H.; Sueyoshi, T.; Miyata, T.; Iwanaga, J.; Rischem. 104, 867-868; 1988
A; Title: A new trisaccharide sugar chain linked to a serine residue in bovine blood coag
A; Rischem 104, 867-868; 1989
A; Contents: amotation
A; Roce: structure and location of covalently bound carbohydrate
A; Roce: structure and location of covalently bound carbohydrate
A; Recerce number: A4556; MUD18921399; PMID: 1349637
A; Roce: structure and location of covalently bound carbohydrate
A; Recerce number: A4556; MUD18921399; PMID: 1349637
A; Roce: structure and location of covalently bound carbohydrate factor
A; Roce: structure and location of covalently bound carbohydrate factor
A; Roce: structure and location of covalently cation of coagulation factor X; Bergertanily; coagulation extrains optimal to accompany to a coagulation carcor X; Roce: Roc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bos primiganius taurus (cattle)
C;Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C;Datession: A31979; C20274
R;Takeya, H; Kawabata, S; Nakagawa, K; Yamamichi, Y.; Miyata, T.; Iwanaga, 8, T. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
A;Reference number: A31979; MUID:89008362; PMID:3049594
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C;Species: Homo sapiens (man)
C;Dare: 30-Nov-1980 #sequence revision 22-Jul-1994 #text change 08-Dec-2000
C;Accession: A29351; A00914; B00914; A37549; A37550; I51952
                                                                          Gaps
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                                                                                                                                                                                                                                                                   ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPODTDVFWAKY 88
                                                                     Indels
                                                                                                                                                           1 ANS-FLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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           Pred. No. 0.00017;
; Mismatches 21
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Pred. No. 0.00013;
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40.0%;
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41.5%;
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Best Local Similarity
Matches 18; Conser
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:336-482,536-550,564-594/Disulfide bonds: #status predicted

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completed: March 1, 2004, 10:10:00
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Job time
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Althernate names: virus-activateing proteinase
C.Species: Gallus gallus (chicken)
C.Species: 12-Feb-1993 #sequence_revision 07-Feb-1997 #text_change 16-Jul-1999
C.Accession: S18938; S20380; S20381
R.Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; NaFES Lett. 283, 281-285, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;241-468/Domain: trypsin homology <TRY>
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;46,47,54,56,59,60,65,66,69,72,75,79/Modified site: gamma-carboxyglutamic acid (Glu) #s
F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
F;196,207,228,285/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;282,328,425/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
Reference number: S20380; MUID:92164779; PMID:1537403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         athway: blood coagulation
uperfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
eywords: beta-hydroxyaspartic acid, beddicted cardo, calcium binding; carboxyglutam
1-40,/Domain: signal sequence #status predicted cardo.
1-40,/Domain: propeptide #status predicted cardo.
1-40,/Domain: gla domain homology cGLA>
1-485/Product: coagulation factor X light chain #status experimental cLCH>
0-121/Domain: EGF homology cEGI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title: Primary structure of the virus activating protease from chick embryo. Its ident
Reference number: S15838; MUID:91257322; PMID:2044767
Accession: S15838
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86-475/Product: coagulation factor X heavy chain #status predicted <HCH>
86-240/Domain: activation peptide #status predicted <APT>
41-475/Product: coagulation factor Xa heavy chain #status experimental <AHC>
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F:391-407/Disulfide bonds: #status experimental
F:464.462/Active alte: His, Asp #status predicted
F:466/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:568/Active site: Ser #status experimental
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idues: 41-55 <GO2>
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Residues: 1~475 <SUZ>
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RESULT S53434

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C;Accession: S53434
R;Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
R;Greengard, J.S.; Fernandez, J.A.; Radtke, K.P.; Griffin, J.H.
B;chem. J. 305, 397-403, 1995
A;Title: Identification of candidate residues for interaction of protein S with C4b bind A;Reference number: S53433; MUID:95134217; PMID:7832752
A;Accession: S53434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom
1-51/Domain: Gla domain homology (fragment) <GLA>
                                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-642 <GRE>
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asma protein S precursor, vitamin K dependent - rhesus macaque (fragment) Species: Macaca mulatta (rhesus macaque)
Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 16-Jul-1999
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Pred. No. 0.00091;
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1-7/Domain: signal sequence (fragment)
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Best Local Similarity 34.19
Matches 15; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 141681 seqs, 52070155 residues
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RRTC_MOUSE
RRTC_PIG
RTC_PIG
RATO_BOVIN
NAIO_HUMAN
MAIO_HUMAN
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HRB_RAT
HRB_RAT
HRB_ROUSE
MG4_HUMAN
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AIO_CALCK
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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P00735 bos taurus Q08761 mus musculu P00744 bos taurus O14669 homo sapien P22891 homo sapien P44647 haemophilus P35916 mus musculu P43068 candida alb P3596 homo sapien Q91086 mus musculu O08775 rattus norv
THRB BOVIN PRIZ_MOUSE PRIZ_BOVIN TMG2 HUMAN PRIZ_HUMAN PRIZ_HUMAN VGR3 MOUSE WKC1_CANAL VGR3 HUMAN VGR1 HUMAN VGR1 HUMAN VF11 HUMAN VF11 MOUSE
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RP	SEQUENCE FROM N.A.
X	MEDLINE=85270390; PubMed=2991887;
RA	r D.C., Yoshitake S., Davie E.W
RT	quence of the
RL	c. Natl. Acad. Sci. U.S.A. 82:467
N.	
RЪ	SEQUENCE FROM N.A.
KX.	15269639; PubMed=2991859;
R.	Beckmann R.J., Schmidt R.J., Santerre R.F., Plutzky J., Crabtree G.R.,
æ	1
RT	"The structure and evolution of a 461 amino acid human protein C
RŢ	ursor and its messenger RNA, based upon
RŢ	,
RL	Nucleic Acids Res. 13:5233-5247(1985).
RN	
RP	SEQUENCE FROM N.A.
X	MEDLINE=86120978: PubMed=3511471;
RA	Plutzky J., Hoskins J.A., Long G.L., Crabtree G.R.,
RT	"Evolution and organization of the human protein C dene.";
RL	-550 (1986).
RN	
C,	SEQUENCE FROM N.A.
RA	Rieder M.J. Carrington D.P. Chung MW. Lee K.L. Poel C.L. Yi O.
RA	
RI	Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN	[2]
유	SEQUENCE FROM N.A.
RC	TISSUE=Colon;
X	MEDLINE=22388257; PubMed=12477932;
RA	E.A., Grouse L.H., Derge J.C
RA	men C.M., Schuler
RA B	, Buetow K.H., Schaefer C.F.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Z.	., Rubin G.M., Hong L.,
R.	., Casavant T.L., Scheetz
КA	S., Carninci P., Prange C
RA	3.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy
Z.	, Malek J.A., Gunaratne P.
Z :	S., Worley K.C., Hale S., Garcia A.M., Ga
\$	VILIAION D.K., Muzny D.M., Sodergren E.U., Lu K., Gibbs K.A.,

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"Protein C deficiency: a database of mutations. For the Protein C & S Subcommittee of the Scientific and Standardization Committee of the International Society on Thrombosis and Haemostasis."; Thromb. Haemost. 69:77-64 (1993).
    Sanchez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8 A crystal structure of Gla-domainless activated protein C.", J. 15:6822-6831(1996).
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Mather I., Oganessyan V., Hof P., Huber R., Foundling S., Esmon C.,
Bode W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Heredicary thrombophilia: identification of nonsense and missense mutations in the protein C gene.";
Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94272342; PubMed-8003977;
Figher C.L., Greengard J.S., Griffin J.H.;
Models of the serine protease domain of the human antithrombotic
plasma factor activated protein C and its zymogen.";
Protein Sci. 3:588-599(1994).
                                                                                                                                                                                                                      MEDLINE=90293094; PubMed=1694179; Miletich J.P., Broze G.J. Jr., "Beta protein C is not glycosylated at asparagine 329. The rate or translation may influence the frequency of usage at asparagine-X-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT PROC DEFICIENCY CYS-444.
WEDDLINE=$72042211, PubMed=437584;
Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Clanetti L.,
Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle C.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                            MEDLINE=92184750; PubMed=1544894;
Harris R.J., Ling V.T., Spellman M.W.;
"O-linked fucose is present in the first epidermal growth factor domain of factor Ib but not protein C.";
J. Biol. Chem. 267:5102-5107(1992).
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Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.
Sala N., Cooper D.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Protein C London 1: recurrent mutation at Arg-169 (CGG-->TGG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grundy C.B., Chitolie A., Talbot S., Bevan D., Kakkar V.V., Cooper D.N.,
                                                                                                                   [6]
SEQUENCE OF 106-461 FROM N.A.
MEDLINE=84272714; PubMed=6589623;
Foster D.C., Davie E.W.;
"Characterization of a cDNA coding for human protein Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 84-461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the protein C gene causing thrombosis."
Nucleic Acids Res. 17:10513-10513(1989)
                                                                                                                                                                                                                                                                            cysteine sites.";
J. Biol. Chem. 265:11397-11404(1990)
                                                                                                                                                                                                             CARBOHYDRATE-LINKAGE SITE ASN-371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [14]
VARLANT PROC DEFICIENCY CYS-272.
MEDLINE=91329836; PubMed=1868249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90098906; Pubmed=2602169;
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                                                                                                                                                                                                                                                                                                                  HYDROXYLATION
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Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.; "The spectrum of genetic defects in a panel of 40 Dutch families with symptomatic protein C deficiency type I: heterogeneity and founder
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MEDLINE-92305321; PubMed-1611081;
Sugahara Y., Miura O., Yuen P., Aoki N.;
"Protein C deficiency Hong Kong 1 and 2: hereditary protein C deficiency caused by two mutant alleles, a 5-nucleotide deletion and a missense mutation.";
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MEDIATE=29276939; PubMed=1593115;
Yamamoto K., Matsubita T., Sugiura I., Takamatsu J., Iwasaki E.,
Wada H., Deguchi K., Shirakawa S., Saito H.;
"Homorygous protein C deficiency: identification of a novel missense
mutation that causes impaired secretion of the mutant protein C.";
J. Lab. Clin. Med. 119:682-689(1992).
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MEDLINE-92380661; PubMed-1511989;
Grundy C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
"Two different missense mutations at Arg 178 of the protein C (PROC)
gene causing recurrent venous thrombosis.";
Hum. Genet. 89:685-686(1992).
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MEDLINE-93271391; PubMed-8499565;
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"Puban Hovel mutations located in exons III and IX of the protein C gene in patients presenting with defective protein C anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
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MEDLINE=93250852; PubMed=1301959;
MEDLINE=93250852; PubMed=1301959;
Gandrille S., Vidaud M., Aiach M., Alhenc-Gelas M., Fischer A.M.,
Gouault-Heilman M., Toulon P., Fiessinger J.N., Goossens M.;
"Two novel mutations responsible for hereditary type I protein C
deficiency: characterization by denaturing gradient gel
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Bertina R.M.;
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"Protein Cvermont: symptomatic type II protein C deficiency associated with two GLA domain mutations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92380660; PubMed=1511988;
Grundy C.B., Chisholm M., Kakkar V.V., Cooper D.N.;
"A novel homozygous missense mutation in the protein C
causing recurrent venous thrombosis.";
Hum. Genet. 89:683-684(1992).
                                                                                                                                                                                                                                  VARIANTS PROC DEFICIENCY ALA-62 AND MET-76 MEDLINE=92190481; Pubmed=1347706;
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VARIANT PROC DEFICIENCY TRP-57.
MEDLINE=93271396; PubMed=8499568;
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Blood 82:159-168(1993).
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                                                                                                                              effects.";
Blood 78:890-894(1991)
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Blood coagulation; Glycoprotein, Serine protease;
Blood coagulation; Glycoprotein, Serine protease;
Gamma-carboxyglutend; calcium-binding; Vitemin K; Hydroxylation;
EGF-like domain; Repeat; Endothelial cell; Hydrolase; Signal.
NON TER 1 1 2 2 BY SIMILARITY.
PRODEP 28 36 BY SIMILARITY.
CHAIN 37 458 VITAMIN K-DEPENDRY PROTEIN C.
CHAIN 37 192 PROTEIN C ILGHT CHAIN (BY SIMILARITY).
CHAIN 195 458 PROTEIN C LICHT CHAIN (BY SIMILARITY).
PEPTIDE 195 209 ACTIVATION PEPTIDE (BY SIMILARITY).
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BY SIMILARITY.
VITAMIN K-DEPENDENT PROTEIN C.
PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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HYDROXILATION (BY SIMILARITY).

CHARGE RELAY SYSTEM.

CHARGE RELAY SYSTEM.

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PÉAM; PF00089; trypsin; 1.
PRINTS; PR00012; CHYMORYPSIN.
PRINTS; PR00012; CHYMORYPSIN.
PRINTS; SW00181; EGF; 2.
SWART; SW00181; EGF; 2.
SWART; SW00020; ELA; 1.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00101; ASX HYDROXYL; 1.
PROSITE; PS00101; EGF_1; 1.
PROSITE; PS001187; EGF_2; 2.
PROSITE; PS001187; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00013; TRYPSIN_LAIS; 1.
PROSITE; PS00135; TRYPSIN_LIS; 1.
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Matches 27; Conservative
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-1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
-1- FTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-1- FTM: The vitamin K-dependent, with stronger affinity to another site, beyond the GlA domain. This GLA-independent binding thrombomodulin complex.
-1- SIMILARITY: Eslorgs to peptidase family S1.
-1- SIMILARITY: Contains 2 EGF-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shen L., He X., Dahlback B.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                       (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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                    86.9%; Score 172; DB 1; Length 461; 75.0%; Pred. No. 5.9e-21; rive 2; Mismatches 9; Indels
                                                                                                            44
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                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vitamin.*Capendent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood
                                                                                                       1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
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InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR00529; EGF_like.
InterPro; IPR005293; GLA_blood.
InterPro; IPR006210; IEGF.
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InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GLA.
Pfam; PP00008; EGF; 2.
Pfam; PP00594; gla; 1.
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HSSP; P04070; 1PCU.
                    Query Match
Best Local Similarity 75.0
Matches 33; Conservative
                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         factor XIV) (Fragment).
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TISSUE=Liver;
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ID PRTC RABIT
AC Q28661;
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-!- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the activated by thrombin, which cleaves a terradecapeptide from the activated by thrombin, this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomcdulin.

-!- ISUB SPECIFICITY: Plasma, synthesized in the liver.
-!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified procein to bind calcium.

-!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified procein to bind calcium.

-!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu stesidues allows the modified procein to bind calcium.

-!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu sessitum also binds, with stronger affinity to another site, beyond the Gla domain. This Gla-independent binding thrombomcdulin complex to peptidase family SI.

-!- SIMILARITY: Contains 2 EGF-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94318474; PubMed=8043441;
Murakawa M., Okamura T., Kamura T., Kuroiwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that
regulates blood coagulation by inactivating factors Va and VIIIa
in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                             P33587; 035498;
01-FEB-1994 (Rel. 28, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SvJ;
MEDLINE=98152576; PubMed=9493582;
Valbert L.R., Rosen E.D., Lissens A., Carmeliet P., Collen D.,
Castellino F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92316897; PubMed=1618739; Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.; "Isolation and characterization of a mouse protein C cDNA."; J. Biochem. 111:491-495(1992).
37 ANSFLEELRPSSLERECVEEVCDLEEAKEIFOSVDDTLAFWYKY 80
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EMBL; D10445; BAA01235.1; -

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Blood coagulation; Glycoprotein; Serine protease;
Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;
EGF-mis Repeat; Endothelial cell; Hydrolase; Signal.
PROPEP 34 81 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                            PROTEIN C LIGHT CHAIN (BY SIMILARITY).
PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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CHARGE RELAY SYSTEM.
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CHARGE RELAY SYSTEM.
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(GAMMA-CARBOXYGLUTAMIC ACID

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EMBL; D43755; BAA07812.1; -.
PIK; JX0210; JX0210.
HSSP; P04070; IPCU.
MEROPS; S01.224 si, -.
MGD; MGI:97711; Proc.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR001801; CQF Ser_Lrypsin.
InterPro; IPR001801; EGF_C.
InterPro; IPR006209; EGF_Like.
                                                                         InterPro; IPR006209; EGF_like.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001214; Peptidase_S1.
InterPro; IPR000294; VitK_dep_GLA.
Fram; PP0000A.
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-!- TISSUE SPECIFICITY: Plana,: synthesized in the liver.
-!- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-!- PTM: another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-thrombomodulin complex.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Wistar; TISSUE=Liver;
MEDIINE=9232550; Pubmed=1627650;
MEDIINE=9232550; Pubmed=1627650;
Marumoto Y.;
"The cDNA cloning and mRNA expression of rat protein C.";
"The cDNA cloning and mRNA expression of rat protein C.";
Biochin. Biochin. Biochin. 1329-332(1992).
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholigids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
                                                                                                                                                       Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                             01-0TJ-1993 (Rel. 26, Created)
01-0TJ-1993 (Rel. 26, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprochrombin IIA) (Anticoagulant protein C) (Blood coagulation PROC.
INTERCHAIN (BY SIMILARITY).
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N-LINKED (GLCNAC. ...) (POTENTIAL).
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MISSING (IN REF. 2).
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PROTEIN C LIGHT CHAIN (BY SIMILARITY)

PROTEIN C HEAVY CHAIN (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).

CLEAVAGE (BY THROMBIN) (BY SIMILARITY).

EGF-LIKE 1.

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EGF-LIKE 2.

EGF-LIKE 1.

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GAMMA-CARBOXYGLUTAMIC ACID
MEROPS; SO1.218; -
InterPro; IPRO00152; Asx_hydroxyl_S.
InterPro; IPRO01080; Cys_Ser_trypsin.
InterPro; IPRO01080; EgF_Cis_
InterPro; IPRO01080; EgF_Cis_
InterPro; IPRO01280; EgF_Like.
InterPro; IPRO01280; Peptidase_S1.
InterPro; IPRO01280; Peptidase_S1A.
InterPro; IPRO01290; Autr_dep_GLA.
Pfam; PPO0089; Erypsin; 1.
Pfam; PPO0089; trypsin; 1.
PRINTS; PRO0001; GLABLOOD.
SMART; SM00109; EGAP_CA; 1.
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                      InterPro; IPR006209; EGF_like.
InterPro; IPR002183; GLA_blood.
InterPro; IPR006210; IEGE
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR000294; VitK_dep_GLA.
      EGF_Ca.
EGF_like.
GLA_blood.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which oleaves a terradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

-1- TISSUE SPECIFICITY: Plasma; synthesized in the liver.
-1- PTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-1- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell. Mol. Life Sci. 58:148-159(2001).
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Liver;
MEDLINE=21121490; PubMed=11229814;
Grimm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of
                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-PEB-2003 (Rel. 41, Last annotation update)
Vicamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
MCBI_TaxID=9823;
  (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL) (GLCNAC. . .) (POTENTIAL)
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                                                                                                 Length 461;
                                                                                                                                      12; Indels
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                                                                                                                                                                         1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
N-LINKED (GLCNAC. . .) (PK
N-LINKED (GLCNAC. . .) (PK
N-LINKED (GLCNAC. . .) (PK
RAACF93664EDACD5 CRC64;
                                                                                               66.7%; Score 132; DB 1; 56.8%; Pred. No. 2.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thrombomodulin complex. SIMILARITY: Belongs to peptidase family S1. SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                 459 AA
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InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR009003; Cys_Ser_trypsin.
                                                                                                                                                                                                                                                                                                                 PRT;
  215 N-
291 N-
355 N-
51912 MW;
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                                                                                                                                    Conservative
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  215
291
355
461 AA;
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                                                                                                                 Similarity
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                  CARBOHYD
CARBOHYD
SEQUENCE
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Best Local
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Vitamin K; Hydroxylation;

SIMILARITY) (BY

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MEDLINE-89213514; PubMed=6406503;
JOHNSON A.E., Esmon N.L., Laue T.M., Esmon C.T.;
Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;
Johnson A.E., Esmon M.L., Laue T.M., Esmon C.T.;
Johnson A.E., Esmon M.L., Laue T.M., Esmon C.T.;

by Ca2+ binding to a high affinity site that does not contain gamma-carboxyglutemic acid.";

carboxyglutemic acid.";

J. Biol. Chem. 258:5554-5560(1983).

-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-83213513; PubMed=6304092;
Bsmon N.L., Debault L.E., Esmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-
                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Evkaryotas, Metazos, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=85014826; PubMed=6091100;
Long G.L., Balagaje R.M., McGillivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bovine protein Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
BY SIMILARITY.

LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)
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SEQUENCE OF 40-194, AND CARBOHYDRATE-LINKAGE SITE ASN-136.
MEDLINE=831007325; PubMed=6896876;
Pernlund P., Stenflo J.;
"Amino acid sequence of the light chain of bovine protein C.'
". Biol. Chem. 257:12170-12179 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83169769; PubMed=6572939;
Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.;
"Bera-hydroxyaspartic acid in vitamin K-dependent protein C."
Proc. Natl. Acad. Sci. U.S.A. 80:1802-1806(1983).
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                                                                        Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND ASN-366.
MEDLINE-83007326; PubMed=6896877;
Stenfilo J. Fernlund P.;
"Amino acid sequence of the heavy chain of bovine protein
J. Biol. Chem. 257:12180-12190(1982).
                                                                                              13; Indels
                                                                                                                                 42 ANSFLEELRPSSLERECKEETCDFEEAREIFONTENTWAFWSKY 85
                                                                                                                   1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                        53 N-LINKED (GLCNAC. . .) (PC
51866 MW; 8541AAC14CC16D09 CRC64;
                                                                      Score 126; DB 1;
Pred. No. 2.9e-13;
                                                             63.6%; Scor.
54.5%; Pred. No. z...
7; Mismatches
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                                                                                                                                                                                                    STANDARD;
396
138
138
292
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353
459 AA;
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AC P00745;
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STRUCTURE BY NWR OF 85-126.
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MEDLINE=84247315; PubMed=6330671;
Fung M.R., Campbell R.M., McGillivray R.T.A.;
"Blood coagulation factor X mRNA encodes a single polypeptide chain containing a prepro leader sequence.";
Nucleic Acids Res. 12:4481-4492(1984);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of the light chain of bovine factor X1 (Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 41-180.
MEDLINE=80130563; PubMed=6766735;
Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
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13-MUL-1987 (Rel. 05, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.1%; Score 115; DB 1; Length 456; 47.6%; Pred. No. 2e-11;
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(GLCNAC. . .).
(GLCNAC. . .).
(GLCNAC. . .).
GAMMA-CARBOXYGLUTAMIC ACGAMMA-CARBOXYGLUTAMIC ACGAMMA-CARBOX RELAY SYSTEM.
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CHARGE RELAY SYSTEM.
BY SIMILARITY.
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MEDLINE-83308813; PubMed-6688526;
McMullen B.A., Fujikawa K., Kisiel W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 47.6 20; Conservative
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                                                                                                                                                                                                                                                                                   253
318
382
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456 AA;
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STRUCTURE BY NMR OF 85-126.
MEDLINE-91084483, PubMed=2261466,
Selander M., Perseon E., Stenflo J., Drakenberg T.;
Selander M., Perseon E., Stenflo J., Drakenberg T.;
"IH NMR assignment and secondary structure of the Ca2(+)-free form of the amino-terminal epidermal growth factor like domain in coagulation factor X.";
                                                                                                                                                                                                                                                                                                                                       chain.";

Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975).

[5]

SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.

MEDIATE=94062825, PubMed=8243461;

Inoue K., Morita T.;

"Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate Eur. J. Biochem. 218:153-163(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=76053121; PubMed=1059122;
Fujikawa K., Titani K., Davie E.W.;
"Activation of bovine factor X (Stuart factor): conversion of factor
Axa-alpha to factor Xa-beta.";
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
                                                                                                                                                         AND DISULFIDE BONDS
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ACTIVE SITE.
ACTINE=7353314; PubMed=4264286;
MEDLINE=7353314; PubMed=4264286;
Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
Neurath H., Davie E.W.;
"Bovine factor X la (activated Stuart factor). Evidence of homology
"Bovine factor X la (activated Stuart factor).
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                                                                                                                                                 SEQUENCE OF 183-492, CARECHYDRATE-LINKAGE SITES, AND DISULFIDE BK
MEDLINE-76053069; PubMed=1059093;
Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
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MEDLINE-92406922; PubMed=1527084;
Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O.,
Stenflo J., Drakenberg T.;
"How an epidermal growth factor (EGF)-like domain binds calcium.
resolution NMR structure of the calcium form of the NH2-terminal
                                                                                                                                                                                                                                                                          'eurath H.;
'Bovine factor X1 (Stuart factor): amino-acid sequence of heavey
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MEDLINE=86140210; PubMed=3949800;
Morita T., Jackson C.M.;
"Localization of the structural difference between bovine blood coagulation factors XI and X2 to tyrosine 18 in the activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Three-dimensional structure of the apo form of the N-terminal BGF-like module of blood coagulation factor X as determined by appertroscopy and simulated folding."; spectroscopy and simulated folding."; slochemistry 31:5974-5983(1992).
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Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
"The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation zymogens."; Biochem. Biophys. Res. Commun. 115:8-14(1983).
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J. Biol. Chem. 261:4008-4014(1986)
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Biochemistry 29:8111-8118(1990).
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                                                                                                                              The relative orientation of Gla and EGF domains in coagulation factor X is altered by Ca2+ binding to the first EGF domain. A combined NMR-small angle X-ray scattering study.";

E slochemistry 35:11547-11559(1996).

-!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

-!- FUNCTION: Pactor Xa is a vitamin K-dependent glycoprotein that calcium and phospholipid during blood clotting.

-!- FUNCTION: Pactor Xa is a vitamin K-dependent by closur thrombin.

-!- FUNCTION: Preferential cleavage: Arg-|-Thr and then Arg-|-II-bonds in prothrombin to form thrombin.

-!- SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.

-!- FUN: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.

-!- FUN: A and O-glycosylated.

-!- FUN: The ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY).

-!- FUN: NESELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain.

-!- SIMILARITY: Belongs to peptidase family S1.
like domain in coagulation factor X.";
J. Biol. Chem. 267:19642-19649(1992).
[13] STRUCTURE BY NNR OF 41-126.
MEDLINE=96387194; PubMed=8794734;
Sunnerlyagen M., Olah G.A., Stenfilo J., Forsen S., Drakenberg T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | PS00022; EGF_1; 1.
| PS01186; EGF_2; 2.
| PS50026; EGF_3; 1.
| PS01187; EGF_CA; 1.
| PS00011; GLU CARBOXYLATION; 1.
| PS002010; TRYPSIN_DOM; 1.
| PS00113; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR009103; Asx hydroxyl s. InterPro; IPR009103; Cyg Ser_trypsin. InterPro; IPR009103; Cyg Ser_trypsin. InterPro; IPR001801; EGF_Ca. InterPro; IPR001801; EGF_Ca. InterPro; IPR001801; EGF_Ca. InterPro; IPR001801; EGF_Ike. InterPro; IPR001801; Peptidase_S1. InterPro; IPR001814; Peptidase_S1A. InterPro; IPR001814; Peptidase_S1A. InterPro; IPR001814; Peptidase_S1A. InterPro; IPR001814; Vitk_dep_Gla. Fean; PF00080; EGF; 2. Fean; PF00080; EGF; 2. Fean; PR00180; EGF; 2. Fean; PR00180; EGF; 3. Fean; PR00180; EGF; 3. Fean; PR00180; EGF; 3. ENRINTS; PR00179; EGF_CA; 1. ERNNTS; SM00069; GLA.; 1.
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3; PS00010; ASX HYDROXYL; 1.
3; PS00022; EGF 1; 1.
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PDB, 1APO, 31-JAN-94.
PDB, 1CCP, 31-MAY-94.
PDB, 1WHE, 15-MAY-97.
PDB, 1IOD, 21-JAN-03.
PDB, 1KIG; 28-OCT-98.
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Glycoprotein, Hydrolase, Serine protease, Plasma, Blood coagulation, Gamma-carboxyglutamic acid, Hydroxylation, Calcium-binding, Vitamin K; Signal; Zymogen, EGF-like domain, Repeat, Sulfation, 3D-structure. 151GNL. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=91216473; PubMed=1902434; Messler T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.; Micloning and expression in COS-1 cells of a full-length cDNA encoding numa coagulation factor N.";
                                                                                                                                                                     ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
MAY BE REMOVED BUT IS NOT NECESSARY FOR
                                                                                                                                                                                                                                             ACTIVATION.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
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TISSUB=Ovary;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
"Gene for human factor X: a blood coagulation factor whose gene
organization is essentially identical with that of factor IX and
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P00742; Q14340;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1089 (Rel. 12, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
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Pred. No. 2.3e-09;
8; Mismatches 18; Indels
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
GANGA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
GAMMA-CARBOXYGLUTAMIC ACID.
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                                                                                                                           FACTOR X LIGHT CHAIN. FACTOR X HEAVY CHAIN.
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Uddin T.B., Toshlyuki S., Carninci P., Prange C.,
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Nilalon D.K., Munny D.M., Sodergran B.J., Lu X., Gibbs R.A.,
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Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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Human and mouse cDNA sequences ",
Fric. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Inoue K., Morita T.;

"Identification of O-linked oligosaccharide chains in the activation

peptides of blood coagulation factor X. The role of the carbohydrate

moleties in the activation of factor X.";

Eur. J. Biochem. 218:153-163(1993).
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MEDLINE=90128299; PubMed=2612918;
Jagadeeswaran P., Reddy S.V., Rao K.J., Hamsabhushanam K., Lyman G.;
"Cloning and characterization of the 5' end (exon 1) of the gene encoding human factor X.";
Gene 84:517-519(1989).
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MEDIINE=86221713; PubMed=3011603;
Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
"Isolation and characterization of human blood-coagulation factor X cDNA.";
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MEDLINE=85216545; PubMed=2582420;
Fung M.R., Hay C.W., Mcdillivray R.T.A.;
Fung M.R., Hay C.W. and the second of 
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McMullen B.A., Fujikawa K., Kisiel W., Sasagawa T., Howald W.N.,
Kwa E.Y., Weinstein B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Padmanabhan K., Padmanabhan K.P., Tulinsky A., Park C.H., Bode Huber R., Blankenship D.T., Cardin A.D., Kisiel W.; "Structure of human des(1-45) factor Xa at 2.2-A resolution.";
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X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
MEDLINE=98283982; PubMed=9618463;
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Leytus S.P., Chung D.W., Kisiel W., Kurachi K., Davie E.W. "Characterization of a cDNA coding for human factor X.";
Proc. Natl. Acad. Sci. U.S.A. 81:3699-3702(1984).
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Padmanabhan K., Padmanabhan K.P.,
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Biochemistry 22:2875-2884(1983).
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                                                                                                                                                                                                                                                                                                                            Nat. Genet. 23:373-373(1999).

Nat. Genet. 23:373-373(1999).

-! FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholishid during blood clotting.

-! CATALYTICA CTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ile bonds in prothrombin to form thrombin.

-! SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or more disulfide bonds.

-! TISSUE SPECIFICITY: Plasma; synthesized in the liver.

-! PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.

-! PTM: N- and O-Glycosylated.

-! PTM: N- and O-Glycosylated.

-! PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY).

-! SIMILARITY: Belongs to peptidase family S1.
                                                                                                                                                                                 "Characterization of single-nucleotide polymorphisms in coding regions
                                                                            VARIANTS ILE-7 AND HIS-30.
MEDILINE=99318093; PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim B.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipsbutz R., Daley G.Q.,
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"Structural basis for chemical inhibition of human blood coagulation
Factor Xa.",
Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
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Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF503510; AAM19347.1; -. BC046125; AAH46125.1; -.
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EMBL; M57285; AAA52421.1; -.
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AAA52636.1;
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23-MAR-99.
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FA10_RABIT
              DOMAIN
TRANSMEM
DOMAIN
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SEQUENCE
                                                                     Query Match
                                                                                Local
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                                                                                                                                                                   FA10_RABIT
                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                  Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 3 precursor.
                                                                                                                        GO; GO:0005576; C:extracellular; TAS.
GO; GO:0003804; F:blood coagulation factor X activity; TAS.
GO; GO:0007596; P:blood coagulation; TAS.
                                                                                                                                                                  Length 488;
                                                                                                                                                                                    18; Indels
                                                                                                                                                                                                                  41 ANSFLEEMKKGHLERECMEETCSYEEAREVFEDSDKTNEFWNKY 84
                                                                                                                                                                                                     1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GG; GO:0016021; C:integral to membrane; NAS.
InterPro; IPR002383; GLA blood.
InterPro; IPR002394; VitK dep_GLA.
PFIM: PF00594; 912; 1.
PRINTS; PR00001; GLABLOOD.
SWART; SM00069; GLA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROPEP 1 19 POTENTIAL.
                                                                                                                                                               Query Match
Best Local Similarity 40.9%; Pred. No. 3.3e-09;
Matches 18; Conservative 8; Mismatches 18.
                                                                                                                                                                                                                                                                         231 AA
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF326350; AAK00955.1; -.
HSSP; P00740; 1CFH.
                                                                                                                                                                                                                                                                        STANDARD;
PDB; 1KSN; 19-JUN-02.
PDB; 1KXF; 11-FEB-03.
PDB; 1MQ6; 28-JAN-03.
PDB; 1MV6; 28-JAN-03.
PDB; 1NFU; 25-FEB-03.
PDB; 1NFY; 25-FEB-03.
PDB; 1NFY; 25-FEB-03.
PDB; 1NFY; 25-FEB-03.
MEXOPS; 201.216; -...
GlycoSuiteDB; P00742; -...
GlycoSuiteDB; P00742; -...
MEM: 13450; -...
                                                                                              HGNC:3528; F10.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carboxylase.
                                                                                                                                                                                                                                                                        HUMAN
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Q9BZD7;
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HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               more disulfide bonds.
-!- PTM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thromb. Res. 85:503-514 (1937).
-!- FUNCTION: Rector Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-Ih bonds in prothrombin to form thrombin.
-!- SUBGNAT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 or
                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:smllarity).
-: PTM: N- and O-glycosylated (By similarity).
-:- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTRINSIC PATHWAY), OR BY FACTOR VILA (IN THE EXTRINSIC PATHWAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain.
-1- SIMILARITY: Belongs to peptidase family S1.
-1- SIMILARITY: Cortains 2 EGF-like domains.
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Pendurthi U.R., Anderson K.D., James H.L.;
"Characterization of a full-length cDNA for rabbit factor X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-CT-2003 (Rel. 42, Least annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor)
                                                                                                                                                                                                                                 Length 231;
                                                                                                                                                                                                                       48.5%; Score 96; DB 1; Length 231 39.0%; Pred. No. 1.4e-08; Vative 8; Mismatches 17; Indels
PROTEIN 3.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryotā; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
GLA-RICH.
                                                                                                                                                                8A373E4848490D81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               20 ANEFLEELRQGTIERECMEEICSYEEVKEVFENKEKTMEFW 60
                                                                                                                                                                                                                                                                                                                                                      1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 AA
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InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001081; EGF_2.
InterPro; IPR001481; EGF_Ca.
InterPro; IPR001488 EGF_II.
InterPro; IPR001483; GGF_II.
InterPro; IPR0015393; GIA_lood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                           20 78 EX.
79 101 PO
102 231 CY.
23 60 GLL
231 AA; 25848 MW; 8
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                                                                                                                                                                                                                                                                                        16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus cuniculus
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                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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187 1
205 2
490 AA;
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    CARBOHYD
CARBOHYD
SEQUENCE
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PATRABIT TO PATRABI
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                                            | Property 
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
SERINE PROTEASE.
GAMMA-CARBOXYGLUTAMIC ACID (BY
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAC.
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InterPro, IPR001254; Peptidase SI.
InterPro, IPR001314; Peptidase SIA.
InterPro, IPR000294; VitK_dep_GLA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A., "Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII.";
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                        FA7_RABIT STANDARD; PRT; 444 AA.
198139; P79224;
01-FBE1996 (Rel. 33, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus (Rabbit).
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
3A39FA85AF2A6D11 CRC64;
                                                                                                                                  ..
                                                                                   Length 490;
                                                                                   Score 95; DB 1; Length 490
Pred. No. 4.9e-08;
B; Mismatches 18; Indels
                                                                                                                                                                          1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                      41 ANSFLEELKKGNLERECMEENCSYEEALEVFEDREKTNEFWNKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.215; -.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR009003; Cya_Ser_trypsin.
InterPro; IPR001981; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thromb. Res. Suppl. 69:231-238(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93190306; PubMed=8383365;
  187 N-
205 N-
53965 MW;
                                                                                      48.0%;
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HSSP; P08709; 1FAK.
                                                                                                        Local Similarity 40.9
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             conversion accelerator).
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DR InterPro; IPR001438; EGF II.

DR InterPro; IPR00229; EGF_like.

DR InterPro; IPR00229; EGF_like.

DR InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR001034; Vitk_dep_GlA.

DR Ffan; PP00008; EGF; 2.

DR Ffan; PP00008; EGF; 2.

DR PRINTS; PR00010; EGFB_COD.

DR PRINTS; PR00010; GLAB_COD.

DR PRINTS; PR00010; GLAB_COD.

DR PRINTS; PR00010; GLAB_COD.

DR PRINTS; PR00001; GLAB_COD.

DR PRINTS; PR000010; ASX_HYDROXYL; 1.

SNART; SM00069; EGF_3; 1.

DR PROSITE; PS001010; ASX_HYDROXYL; 1.

DR PROSITE; PS01018; EGF_3; 1.

DR PROSITE; PS01018; EGF_3; 1.

PROSITE; PS01018; EGF_3; 1.

PROSITE; PS01018; TRYPEIN DOM; 1.

PROSITE; PS010135; TRYPEIN DOM; 1.

PROSITE; PS010135; TRYPEIN BER; 1.

PROSITE; PS010134; TRYPEIN BER; 1.

PROSITE; PS010134; TRYPEIN BER; 1.

PROSITE; PS010134;
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EGF-LIKE 2.

SERINE PROTEASE.

CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROWBIN) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

SUBSTRATE (BY SIMILARITY).

BY SIMILARITY.

GAMMA-CARBOXYGLUTAMIC ACID.

GAMMA-CARBOXYGLU
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47.5%; Score 94; DB 1; Length 444;
Best Local Similarity 43.9%; Pred. No. 6.5e-08;
Matches 18; Conservative 5; Mismatches 18; Indels
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FACTOR VII HEAVY CHAIN.
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STRUCTURE OF CARBOHYDRATE ON SER-112.
MEDINE-91344709, Pulmbdca-2129367,
IWanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
"A new trisaccharide sugar chain linked to a serine residue in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89088153; PubMed=3264725;
Thim L., Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U.;
"Amino acid sequence and posttranslational modifications of human factor VIIa from plasma and transfected baby hamster kidney cells.";
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                                                                                         TATUMAN STANDARD; PRT; 466 AA.

ID FA7 HUMAN STANDARD; PRT; 466 AA.

ID FA7 HUMAN STANDARD; PRT; 466 AA.

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 01-JAN-1988 (Rel. 42, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin DE Comversion accelerator) (Eptacog alfa).
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MEDLINE-90062160; PubMed=5511201;
MISHIMURA H., Kawabata S.,
Shimonishi Y., Iwanaga S.;
Shimonishi Y., Iwanaga S.;
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[1] Biol. Chem. 264:20320-20325(1989).
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MEDLINES-87860948 PubMed=3037537;
O'Hara P.J. Grant F.J. Haldeman B.A., Gray C.L., Insley M.Y.,
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vitamin K-dependent protein participating in blood coagulation.";
Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
                                                                                                                                                                                                                                                                                                             Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=91250411; PubMed=1904059;
Bjoern S., Foster D.C., Thim L., Wiberg F.C., Christensen M.,
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glycosylations at serine residues 52 and 60 and effects of site-
directed mutagenesis of serine 52 to alanine.";
J. Biol. Chem. 266:11051-11057(1991).
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40 ANSFLEELRPGSLERECKBELCSFEEARBVFQSTERTKQFW
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TISSUE=Liver;
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seq1-32glu-33asp.rsp

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first EGF-like domain of clotting factors VII and IX and protein Z.", Adv. Exp. Med. Biol. 281:121-131(1990).
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MEDINE-2934004; Pubmed=1634227;
MATCHELLIG G., PATROCCHINI P., Gemmati D., Derosa V., Pinotti M.,
Rodorigo G., Casonato A., Girolami A., Bernardi F.;
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Bernardi F., Castaman G., Redaelli R., Pinotti M., Lunghi B.,
Rodeghiero F., Marchetti G.;
"Topologically equivalent mutations causing dysfunctional coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94264305; PubMed=8204879; Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W., Roberts H.R., Blajchman M., Monroe D.M., High K.A.; "Severe factor VII deficiency caused by mutations abolishing the Cleavage site for activation and altering binding to tissue factor."; Blood 83:3524-3535(1994).
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Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N.,
Von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H.,
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polymorphism (SSCP) analysis in five dysfunctional variants of
coagulation factor VII.";
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Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi Marchetti G., Ferrati M., Patracchini P., Redaelli R., Bernardi M. a missense mutation (1780ys---Tyr) and two neutral dimorphisms (115His and 333Ser) in the human coagulation factor VII gene."; Hum. Mol. Genet. 2:1055-1056(1993).
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                                                                                                                                       MEDLINE=96175641; PubMed=8598933;
Banner D.W., D'Arcy A., Chene C., Winkler F.K., Guha A.,
Konigsberg W.H., Nemreson Y., Kirchhofer D.;
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VIIa with soluble tissue factor.";
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BEDLINE-28367502; PubMed=9692950;
Muranyi A., Finn B.E., Gippert G.P., Forsen S., Stenflo J.,
Drakenberg T.;
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MEDLINE=91300046; PubMed=2070047;
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Blood 78:132-140(1991)
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"Characterization of single-nucleotide polymorphisms in coding regions
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the signal sequence identified in a patient with factor VII
deficiency.";
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"A Thr359Net mutation in factor VII of a patient with a hereditary deficiency causes defective secretion of the molecule.";
Blood 87:5085-5094 (1996).
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Alshinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
"Two new missense mutations (P134T and A244V) in the coagulation
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Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
Suzuki K.;
                                                                                                                                                                                                                                                                           "Factor VII Mie: homozygous asymptomatic type I deficiency an amino acid substitution of His (CAC) for Arg(247) (CGC) catalytic domain.";
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Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato
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factors VII (294Ala-->Val) and X (334Ser-->Pro).";
Hum. Mol. Genet. 3:1175-1177(1994).
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MEDLINE=99318093; PubMed=10391209;
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MEDLINE=97037613; PubMed=8883260;
                                                                                                                                                                                                                                                                                                                                                                      Thromb. Haemost. 71:773-777(1994)
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Nat. Genet. 22:231-238(1999).
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Hum. Mutat. 8:108-115(1996)
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VARIANT MORIOKA PRO-13.
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RESULT 13 TMG1_HUMAN

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0
                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein l precursor (Prolinerich Gla protein 1) (Proline-rich Gamma-carboxyglutamic acid protein
                                                                                                                                                                                                                                 MEDLINE=97404347; PubMed=9256434;

Kulman J.D., Harris J.E., Haldeman B.A., Davie B.W.;

Kulman J.D., Harris J.E., Haldeman B.A., Davie B.W.;

Kulman J.D., Harris J.E., Haldeman B.A., Davie B.W.;

Record Structure and tissue distribution of two novel proline-rich gamma-carboxyglutamic acid proteins.";

Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).

-: TISSUB SPECIFICITY: Highly expressed in the spinal cord.

-: TISSUB SPECIFICITY: Highly expressed in the spinal cord.

-: PTM: Gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ANGFFEEIRQGNIERECKEEFCTFEEAREAFENNEKTKEFWSTY 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-PRO.
26538A61AB0AEB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN 1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gamma-carboxyglutamic acid; Vitamin K; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HONC:9469; -PRRGI.

MIM; 604428; -0.

InterPro; IPR000298; Gia, blood.

InterPro; IPR000294; Vitx dep_Gia.

Pfam; PP00594; gla; 1.

PRINTS; SM00069; Gla; 1.

PROSITE; PS00001; GLABLODD.

PROSITE; PS000011; GLU_CARBOXYLATION; 1.
218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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106 POY
218 CY.
61 GL
135 POI
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HSSP; P00740; 1CFH.
STANDARD;
                                                                                                                              PRRG1 OR TMG1 OR PRGP1.
                                                                                                                                                    (Human)
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Best Local Similarity
There 15; Conserva
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84 1
107 2
24
131 1
                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                      Homo sapiens
IMG1 HUMAN
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TRANSMEM
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SEQUENCE
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CHAIN
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P18292; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Prothrombin precursor (EC 3.4.21.5).

GE PT PT BE

RESULT 14 THRB_RAT ID THRB_RAT

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RA Banfield D.K., Macgillivray R.T.;

Raffield D.K., Macgillivray R.T.;

Raffield D.K., Macgillivray R.T.;

Raffield D.K., Macgillivray R.T.;

RT and ifferent species.";

RT nime different species.";

Proc. Natl. Acid. Sci. U.S.A. 89:2779-2783(1992).

- !- FUNCTION: THROMBIN, WHITH CLEAVES BONDS AFTER RG & LVS, CONVERTS

C. - CATALITOR: THROMBON, WHITH CLEAVES BONDS AFTER RG & LVS, CONVERTS

FIRRINGERN TO FIBRIN AND ACTIVATES RACTORS V, VII, VIII, XIII,

AND, IN COMPLEX WITH THROMBONDULIN, PROTEIN C.

- CATALITIC ACTIVITY: Preferential cleavage: Arg-1-Gly; activates

fibringen to fibrin and releases fibrinopeptide A and B.

- - PTM: THE GAMMA-CARBOXYLLATION OF GLUTAMYL RESIDUES WA MICROSOMAL

C. - PTM: THE GAMMA-CARBOXYLLATION OF GLUTAMYL RESIDUES WA MICROSOMAL

ERSULT FROM THE CARBOXYLLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL

C. - PTM: THE GAMMA-CARBOX GLUTAMYL RESIDUES, WHICH IS ESSENTIAL FOR THE CONVERSION

C. - PROTHROMBIN TO THROMBIN.

C. - PROTHROMBIN TO THROMBIN.

C. - MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A

PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &

C. PACTORS VA & AX AN IN CA-DEPRINENT INTERACTIONS; PACTOR XA REMOUSES

THE ACTIVATION PREPIDE & CLEAVES THE REMAINING PART INTO LIGHT &

HEAVY CHAINS: THE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF

THOMBAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANBOUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; DTR009003; Cys Ser trypsin.
InterPro; IPR002383; GLA_blood.
InterPro; IPR002383; GLA_blood.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00294; vitk_dep_GLA.
Pfam; PF00594; gla; 1.
Pfam; PF00594; gla; 1.
Pfam; PF00051; kringle; 2.
Pfam; PR0089; trypsin; 1.
PRNNTS; PR00010; GLABLOOD.
PRINTS; PR00010; GLABLOOD.
PRINTS; PR00011; GLABLOOD.
                                                                                                                                                                                             "cDNA sequence of rat prothrombin.";
Nucleic Acids Res. 18:4251-4251(1990)
                                                                                                                             STRAIN=Sprague-Dawley; TISSUE=Liver;
MEDLINE=90332426; PubMed=2377469;
Dihanich M., Monard D.;
                                                                                                                                                                                                                                                        SEQUENCE OF 383-617 FROM N.A.
TISSUE-Liver;
MEDLINE-92212913; PubMed=1557383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X52835; CAA37017.1; -. EMBL; M81397; AAA42240.1; -. PIR; S10511; S10511. HSSP; P00734; IUVS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0018; KRINGLE.
PRINTS; PRO1505; PROTHROMBIN.
ProDom; PD000395; Kringle; 2.
SMART; SM00069; GLA; 1.
                                                                                                         SEQUENCE FROM N.A
                                                                  NCBI_TaxID=10116;
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SMART; SM00020; TTYP_SPC; 1.

PROSITE; PS00011; GIJ CARBOXYLATION; 1.

PROSITE; PS00021; KRINGLE 1; 2.

PROSITE; PS5020; KRINGLE 2; 2.

PROSITE; PS50240; TRYPSIN DOM; 1.

PROSITE; PS00134; TRYPSIN HIS; 1.

Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat; Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver; Vitamin K; Serine protease; Kringle; Signal.

1 24 portease; Signal.
                                                                                                                                                                                                                 CLEAVAGE (BY THROMBIN).
CLEAVAGE (BY FACTOR XA).
CHAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
CHARGE RELAY SYSTEM (BY SIMILARITY)
                                                                                                                                                                                                                                                                            GAMMA-CARBOXYGLUTAMIC ACID.
MALINKED GICNAC. ) (POTEN
N-LINKED GICNAC. ) (POTEN
N-LINKED GICNAC. )
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KRINGLE 2.
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CLEAVAGE (BY THRO
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SIMILARITY.
SIMILARITY.
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N-LINKED
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560
617 AA;
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CARBOHYD
CARBOHYD
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ä Gaps Ĥ Score 78.5; DB 1; Length 617; Pred. No. 3.7e-05; 5; Mismatches 21; Indels ||| || || :| || :| |:|:|
ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88 1 ANS-FLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44 5; Mismatches 39.6%; Conservative Local Similarity 18; Best Loca Matches ઠે

(Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 43, Last annotation update)
precursor (EC 3.4.21.5). STANDARD; 01-NOV-1990 (Rel. 16, Cz 01-NOV-1990 (Rel. 16, La 15-MAR-2004 (Rel. 43, La Prothrombin precursor (F F2 OR CF2. THRE MOUSE ID THRE MOUSE AC P19221; ON DATE OF THE OFFI

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RN SCOURINGE FROM N.A.

RN SEQUENCE FROM N.A.

RY SEQUENCE T. Secberg B.D. Grouse D.H., Derge J.G.,

RA Altschul S.F., Zecberg B., Butchen E., Shamen C.R., Schuler G.D.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Hopkins R.F., Jordan T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Wokewan R.J., Mallahy S.J.,

RA Bosak S.A., McEwan P.J., McKerman K.J., Malek J.A., Glubs R.A.,

RA Nilalon D.K., Muzzy D.M., Sodergen B.J., Lu X., Glubs R.A.,

RA Nilalon D.K., Muzzy D.M., Madan A., Robigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length

RI human and mouse CDNA sequences.",

171

171
                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                          Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G., Firzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W., "Characterization of the CDNA coding for mouse prothrombin and localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
                                                                            SEQUENCE FROM N.A.
STRAIN-CS7BL/6; TISSUB-Liver;
MEDLINE-91025551; PubMed-2222810;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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SEQUENCE OF 384-618 FROM N.A.

of thrombin.
MISCELLANEGUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation by factor Xa.

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                                                                         | BERIL X52200; CAA36548.1. | BERIL X52200; CAA36548.1. | BERIL X52200; CAA36548.1. | BERIL MERGES; AAA40335.1. | BERIL MERGES; AAA4035.1. | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLEAVAGE (BY THROWBIN).
CLEAVAGE (BY PACTOR XA).
CLEAVAGE (BY PACTOR XA).
CLEAVAGE (BY PACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
GAWMA-CARBOXYGLUTAMIC ACID.
BY SIMILARITY.
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DISULPID
DISULPID
DISULPID
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79 47 91 22 N 44 N N 13 N N N N N N 13 53 N N-1	Query Match Best Local Similarity 40.0%; Pred Matches 18; Conservative 5; Mis Qy ANS-FLXXLRHSSLXRXCIXXICDFXX Qb
333 479 338 5404 551 591 122 122 142 144 1413 413 413 413 553 553 553	39. Conservative 40. Conservative NNS-FLXXLRHSSLX
FT DISULPID FT DISULPID FT DISULPID FT CARBOHYD FT CAR	Query Match Best Local Similarity Matches 18; Conserv Qy 1 ANS-FLXXLR Db 44 ANSGFLEELE Db ' A44 ANGGFLEELEL Search completed: March Job time : 11.5 secs

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March 1, 2004, 09:55:12; Search time 37.5 Seconds (without alignments) 370.208 Million cell updates/sec
                                                                                                                                                              SEQ1-32GLU-33ASP
198
1 ANSFLXXLRHSSLXRXCIXX......XXAKXIFedVDDTLAFWSKH 44
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                               1017041 segs, 315518202 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_rodent:*
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sp_bacteria:*
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sp_human:*
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sp_phage:*
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                   Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ogttro canis famil	O91wn8 mus musculu	Q8j002 homo sapien	Osixbs homo sapien	099pce mus musculu	063207 rattus norv	O7sy86 xenopus lae		O7sxh8 brachydanio	Q8jhc9 brachydanio	Q8n2n6 homo sapien	O80v26 mus musculu	O7t3b6 brachydanio	O54740 mus musculu		
SUMMARIES	ΙD	Q9TTR0	Q91WN8	Q8J002	QBIXBS	923660	063207	Q7SY86	Q804X5	Q7SXH8	Q8JHC9	Q8N2N6	O80Y26	Q7T3B6	054740	Q99L32	088947
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ф	Query Match	72.7	67.2	65.7	65.7	64.1	54.0	51.5	50.5	49.5	48.7	48.5	47.0	47.0	47.0	47.0	47.0
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	Result No.	1	7	m	4	w	ø	7	00	σι	10	11	12	13	14	15	16

Q96pq8 homo sapien		O94md9 ornithorbyn	OBij40 xenopus lae	Q8nek6 homo sapien	Q804x7 qallus qall	fudur	ø	Q15253 homo sapien	Q7z7p3 homo sapien	9	Q804w9 fugu rubrip	homod	016519 homo sapien	ОШО	Q61109 mus musculu	aloc	Q28994 sus scrofa	Q804x2 fugu rubrip	н	Q95nd7 pan troqlod	-	, w	do bra		Д	Q8ixd5 homo sapien	Q804x0 fugu rubrip
Ů.	3 Q8JHC8	0	.3 Q8JJ40	Q8NEK6	.3 Q804X7	.3 Q804W7		015253	Q7Z7P3	.3 Q804X6		072715	016519	00SN6O	1 Q61109	QST613	028994	.3 Q804X2				Q29094	3 Q8JHD0	3 Q90YK1	u	QBIXDS	3 Q804X0
679	474	469	229	268 4	425	612 1	446 1	100	622 4	471 1	475 1	497 4	650 4	650 4	446 1	542 5	138 6	441 1	607 1		461 6	648 6	433 1	433 1	49 6	52 4	430 1
46.5	44 4.4	6.8	41.4	40.9	40.4	40.4	39.9	38.4	38.4	37.4	37.4	37.4	37.4	37.4	36.9	36.1	35.9	35.9	35.4	34.8						33.3	32.3
92	2 2 2 3 4	87	82	81	80	80	79	16	96	74	74	74	74	74	73	71.5	71	71	70	69	69	67		ġ.	99	99	64
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busharyota: Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 65.7%; Score 130; DB 4; Length 55; Best Local Similarity 70.3%; Pred. No. 2.2e-14; Matches 26; Conservative 2; Mismatches 9; Indels
R PEAM; PF00008; EGF; 2.

R PEAM; PF00594; gla; 1.

R PRINTS; PR00199; trypein; 1.

R SMART; SM00109; GLAELCOD.

R SMART; SM00109; GLA; 1.

R SMART; SM00020; Tryp SPc; 1.

R SMART; SM00020; Tryp SPc; 1.

R PROSITE; PS00106; BGF=1; 1.

R PROSITE; PS001186; BGF=2; 2.

R PROSITE; PS00110; GLAELCARBOXYL; 1.

R PROSITE; PS00111; GLU-CARBOXYL; 1.

R PROSITE; PS00113; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN HIS; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R PROSITE; PS00135; TRYPSIN SER; 1.

R EGF-1ike domain; Hydrolae; Protease; Serine protease.

S ERQUENCE 460 AA; 51818 MW; 0117F26E68FCC274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRHSSLXRXCIXXICDFXXAXXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 ANSFLEEMRPGSLERECMERICDFERAQEIFQNVEDTLAFWIKY 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8J002 PRELIMINARY; PRT; 55 AA.
Q8J002;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Protein C (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDT 37
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QBIXBS
ID QBIXI
AC QBIXI
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Q8J002
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              | TheeFPC: 1PR006210; 19R06210; 1PR006210; 1PR066110; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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12.7%; Score 144; DB 6; Length 456;
Local Similarity 61.4%; Pred. No. 9.3e-16;
les 27; Conservative 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 ANSFLEEIRAGSLERECMEEICDFEEAKEIFQNVDDTLAYWSKY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to protein C.
     IPR002383; GLA blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Q91WN8;
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Matches
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482 AA
                 InterPro; IPR000294; VitK_dep_GLA
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Q63207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Hamasaki S., Kang D., Kinoshita S., Iida K., Inoue S., Watanabe K.,
A Kurihara M., Wada Y., Ono M.;
Tarian M., Wada Y., Ono M.;
Tarian analysis of anticoagulation factors in Japanese thrombotic
Unit of the selection of thrombophilia in Japanese thrombotic
Unit of the selection of thrombophilia in Japanese.
Unit of the selection of the selection of thrombophilia in Japanese.
Unit of the selection of the selectio
                                                                                                          Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCPI_TaxID=10090;
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Local Similarity 70.3%; Pred. No. 2.2e-14;
Les 26; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Korf I.;
"Complete sequence of UC72A01.";
"Complete sequence of UC72A01.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
EMBL; AF318182; AAK07918.1;
HSSP; P04070; LAUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD, MGI:9771; Proc.

GO; GO:000550; C:extracellular; IEA.

GO; GO:000550; F:calcium ion binding; IEA.

GO; GO:000823; F:calcium ion binding; IEA.

GO; GO:0004295; F:crypein activity; IEA.

GO; GO:0004295; F:trypein activity; IEA.

GO; GO:0004295; F:trypein activity; IEA.

GO; GO:0006509; F:trypein activity; IEA.

GO; GO:0006509; F:trypein activity; IEA.

GO; GO:0006509; F:trypein activity; IEA.

InterPro; IPR001012; Asx hydroxyl S:

InterPro; IPR0010181; EGF Ca.

InterPro; IPR001283; GLA_lood.

InterPro; IPR001284; Peptidase SI.

InterPro; IPR001284; Peptidase SIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 55 38.3803696534BC9289 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099PG6;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
PROC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDT 37
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                                                                  Protein C (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=C57BL;
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Q99PC6
ID Q99P
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RC SEQUENCE FROM N.A.

RC SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RE SEQUENCE FROM N.A.

REDIINE=96093366; PubMed=8578539;

REDIINE=96093366; PubMed=8578539;

REDIINE=96093366; PubMed=8578539;

RT Carboxylaeu.

RT Carboxylaeu.

RT Carboxylaeu.

RT Carboxylaeu.

RT Carboxylaeu.

RT Carboxylaeu.

RE Thromb. Res. 80:63-73(1958).

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

BR MIL X798077; CAA56202.1; -.

BR MIL X798077; CAA56202.1; -.

BR MENSPP; PO0742; IXKA.

BR MENSPP; PO0742; IXKA.

BR GO: GO:0005576; C: extracellular; IEA.

BR GO: GO:0005509; F: calcium ion binding; IEA.

BR GO: GO:0005509; F: calcium ion
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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| Pfam; PF000894; GGF; 2. | Pfam; PF000894; GGF; 2. |
| Pfam; PF000894; GGF; 2. |
| Pfam; PF000894; GGF; 1. |
| PRINTS; PR000892; CHYMOTRYPSIN. |
| PRINTS; PR000192; CHYMOTRYPSIN. |
| PRINTS; PR00019; GGF CA; 1. |
| SMART; SM00020; GLA; 1. |
| R PROSITE; PS00100; ASK HYDROXYL; 1. |
| R PROSITE; PS001186; EGF C; 2. |
| R PROSITE; PS001186; EGF C; 2. |
| R PROSITE; PS00119; GGF CA; 1. |
| R PROSITE; PS00119; GGF CA; 1. |
| R PROSITE; PS00119; HYPSIN DOM; 1. |
| R PROSITE; PS00134; TRYPSIN HIS; 1. |
| R PROSITE; PS001345 TRYPSIN HIS; 1. |
| R PROSITE; PS001345 TRYPSIN HIS; 1. |
| R PROSITE; PS001345 TR
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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RESULT 8'
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Habet F.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Botheron M., Soars M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Rapleton M., Usdin T.B., Toophlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wishin T.B., Toophlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raha S.S., Worley K.C., Hale S., Garchinci A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodiguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
T. "Genztation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Senopus laevis (African clawed frog).
Bukaryora, Metazod; Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea; Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Whole,
MEDLINE=22341132, PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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Best Local Similarity 40.9%; Pred. No. 1.9e-09;
Matches 18; Conservative 9; Mismatches 17; Indels (
                                                                              PRINTS; FRONCES; DEFENCED.

SWART; SMOO19; EGF CA; 1.

SMART; SMOO19; EGF CA; 1.

SMART; SMOO10; Tryp SPC; 1.

SMART; SMOO10; Tryp SPC; 1.

PROSITE; PS0010; ASX HYDROXL; 1.

PROSITE; PS001187; EGF 2; 2.

PROSITE; PS001187; EGF CA; 1.

PROSITE; PS001187; TRYPSIN HIS; 1.

PROSITE; PS001187; TRYPSIN HIS; 1.

PROSITE; PS001187; TRYPSIN SER; 1.

PROSITE; PS001187; TRYPSIN SER; 1.
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                              PRINTS; PR00722; CHYMOTRYPSIN,
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiative.";
Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   975Y86
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Gallus gallus (Chicken).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davidson C.J., Hirt R.P., Lal K., Shell P., Elgar G.,
A Tuddenham E.G.D., McVey J.H.;
Tuddenham E.G.D., McVey J.H.;
Tuddenham E.G.D., McVey J.H.;
Toomparative sequence analysis and molecular veolution of blood
T coagulation genes from Gallus gallus and Fugu rubripes.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
I Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005509; F:calculum ion binding; IEA.
R GO; GO:0004263; F:chymorrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:0005509; F:trypsin activity; IEA.
R GO; GO:0005509; F:trypsin activity; IEA.
R InterPro; IPR000742; BGF_2.
R InterPro; IPR000742; EGF_2.
                                                                                                                                                                                             ô
                                                                                                                                                        Match 51.5%; Score 102; DB 13; Length 455; Local Similarity 47.7%; Pred. No. 1.3e-08; Los 21; Conservative 6; Mismatches 17; Indels C
                                                                                                                                                                                                                          1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                            49 AFNFMEELKPGSLERECIEEKCDFEEAFEIFETKEDTLNFWAKY 92
                                                Klein S., Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO54968; AAH4968.1; -.
Hypothetical protein.
SEQUENCE 455 AA; 51811 MW; 07C027ED2B495330 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Anticoagulant protein C precursor (EC 3.4.21.69).
                                                                                                                                                                                                                                                                                                                                                     433 AA
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PSO011; GLU CARBOXYLATION; 1.
PSO0240; TRYESIN DOM; 1.
PSO0134; TRYPSIN_HIS; 1.
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nterPro; IPR001314; Peptidase_SlA.nterPro; IPR000294; Vitk_dep_GLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERIO'S TRANCH'S BGF Ca.
INTERPRO'S IPRO01881; BGF Ca.
INTERPRO'S IPRO0209; BGF Tike.
INTERPRO'S IPRO06210; BGF Dood.
INTERPRO'S IPRO01254; Peptidase_S1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100020; Tryp SPc; 1.
PS00010; ASX HYDROXYL;
PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam, PF00089, LTYDSin, 1.
PRINTS; PR00722; CHYMOTRXPSIN.
PRINTS; PR00001; GLABLOOD.
SWART; SM00181; BGF, 2.
SWART; SM00199; BGF CA; 1.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00594; gla; 1
[3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9031;
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SMART; SM00069;
SMART; SM00020; 1
                                   TISSUE=Whole;
                                                                                                                                                      Query Match
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PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                Q804X5;
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Matches
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S X X

RESULT 9 Q7SXH8

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[1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Hanumanthaiah R., Day K., Jagadeeswaran P.;
Hanumanthaive analysis of blood coagulation pathways in Teleostei:
"Comprehensive analysis of blood coagulation of zebrafish
Evolution of coagulation factor genes and identification of zebrafish
       01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Coagulation deactor VIII.
Barachydanio rezio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
48.7%; Score 96.5; DB 13; Length 443;
Best Local Similarity 45.2%; Pred. No. 1.1e-07;
Matches 19; Conservative 7; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                             GO: GO:0005566; G:extracellular; IEA.
GO: GO:0005566; G:extracellular; IEA.
GO: GO:0004265; F:chynctrypsin activity; IEA.
GO: GO:0004295; F:chynctrypsin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
GO: GO:000508; P:proteclysis and peptidolysis; IEA.
INTERPO: IPRO0003; Cyg.Ser.trypsin.
INTERPO: IPRO00043; EGF.2.
INTERPO: IPRO00443; EGF.2.
INTERPO: IPRO00509; EGF.like.
INTERPO: IPRO02509; EGF.like.
INTERPO: IPRO02509; EGF.like.
INTERPO: IPRO0254; Peptidase SI.
INTERPO: IPRO0124; Peptidase SI.
INTERPO: IPRO0114; Peptidase SI.
INTERPO: IPRO0114; Peptidase SIA.
INTERPO: IPRO00594; VITK. dep.GLA.
PFam: PP00008; EGF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Protease, Serine protease. A; 48823 MW; 2D2504718AE94FF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANS-FLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 ANSGFLEEMKAGNLERECVEEICDYEEAREVFEDDDRTKQFW 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein FLJ90093.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                  Factor VIII.";
Blood Cells MOJ. Dis. 0:0-0(2002).
Blood Cells MOJ. Dis. 0:0-0 EPTIDASE FAMILY SI.
EMBL; AFSISS46; AAM8342.1;
EMBL; AFSIS269; AAN71000.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DR PROSITE; PS00022; EGF 1; 1.

DR PROSITE; PS01186; EGF 2; 1.

R PROSITE; PS00011; GLU_CARBOXYLATION; 1.

R PROSITE; PS00013; TRYPSIN DOM; 1.

R PROSITE; PS00134; TRYPSIN_HIS; 1.

R EGF-like domain; Hydrolase: n.
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PRINTS; PR00001; GLABLOOD.
SMART; SM00181; EGF; 2.
SMART; SM00179; EGF CA: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00181; EGF; 2.
SMART; SM00179; EGF_CA; 1.
SMART; SM00069; GLA; 1.
SMART; SM00020; Tryp SPC; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Pfam; PF00089; trypsi:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8N2N6;
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08N2N6
ORNZN
AC 08N2N
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DT 01-0C
DT NOOUS
CO MAMMA
OX NCBI
RN (13)
RP SEQUE
              g
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Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Alaschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahar N.K.,
A both of the colling R.D., Both of the colling B.D., Scheetz T.B.,
A Brownstein M.J., Usdin T.B., Toothyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toothyuki S., Carninci P., Prange C.,
A Bosak S.A., McKennan K.J., Malek J.A., Gunaratne P.H.,
A Brownstein M., Sodergren E.J., Lu X., Gibbs R.A.,
A Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Helton B.K., McKernan M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                              ö
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                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Cramiata, Verrebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae; Danio.
NCBI_TaxID=7955,
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                                                                                       Score 100; DB 13; Length 433;
Pred. No. 2.6e-08;
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                                                                                                                                                                             1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                   40 ANSFLEELKPGSVERECNEERCNFEEASEIFETKEATLEFWSKY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC055596; AAH55596.1; -.
Hypothetical protein.
SEQUENCE 524 AA; 59560 MW; 1B4AE08119080325 CRC64;
                                             433 AA; 48689 MW; E09DDEE56D7DA2A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                            524 AA
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                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Body;
MEDLINE=22388257; PubMed=12477932;
PROSITE; PS00135; TRYPSIN_SER; 1.
                                                                                     Query Match
Best Local Similarity 47.7%;
Matches 21; Conservative E
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Les 18; Conserva
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                                             SEQUENCE
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Gaps

Best Loca Matches

RESULT 10

ОВЛНС9

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Q7T3B6
Q7T3B6;
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Q7T3B6
                      DAR HER BERNELL BERNEL
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XX DINGELING-2338825; PubMed=1247793;

XX STRAIN-CSTBL/63; TISSUE=Embryo;

XX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XI Stander R.D., Collins F.S., Wagner L., Shammen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hasher F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Staplecon M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Mazny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards M.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley W., Helton B. Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley W., Helton B., Ketteman M., Mors R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                           Liborate annuaryo, the subject of 
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
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48.5%; Score 96, DB 4; Length 231,
Best Local Similarity 39.0%; Pred. No. 6.3e-08;
Matches 16; Conservative 8; Mismatches 17; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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01-JUN-2003 (TrEMBLrel. 24, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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STRAIN-C57BL/6J; TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F10 protein.
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Q80Y26
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Attachberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Attacher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Braheton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Romstein M.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Lu X., Gabbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzuny D.M., Sodergren E.J., Lu X., Gabbs R.A.,
Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Annes S.J., Marras M.A.,
June S.J., Marras M.A.,
June R.J., Marras M.A.,
June M. Schein J.E.,
June S.J., Marras M.A.,
June M. Gay L.J., Hulk M. J. R.,
June S.J., Marras M.A.,
June R.J., Marras M.A.,
June M. June R.J., Marras M.A.,
June R.J., Marras M.A.,
June M. June R.J., Marras M.A.,
June R.J., Marras M.A.,
June M. 
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
14/pothetical protein.
15/pothetical protein.
15/pothetical metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes, Cyprinidae; Danio.
NCBI_TaxID=7955;
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36.4%; Pred. No. 3.1e-07;
ive 9; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00069; GLA; 1.
PROSITE; PS0010; ASX HYDROXYL; 1.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; TXPECIN DOM; 1.
PROSITE; PS0134; TRYPEIN HIS; 1.
SEQUENCE 340 AA; 38359 WW; EE252D6157720811 CRC64;
04295; F:trypsin activity; IEA.
65608; P:proteolysis and peptidolysis; IEA.
IPR000162; Asx.hydroxyl_S.
IPR00003; Cys.Ser_trypsin.
IPR000742; EGF_2.
                                                                                                                            InterPro; IPRO00013; Cys_Ser_trypsin InterPro; IPR001013; Cys_Ser_trypsin InterPro; IPR001013; EGF_Ca.
InterPro; IPR001013; EGF_Ta.
InterPro; IPR001013; EGF_Ti.
InterPro; IPR00209; EGF_Ti.
InterPro; IPR00210; IEGF_Ti.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001294; VitK_dep_GLA.
Pfam; PR00109; EGF; 2.
Pfam; PR00109; EGFBLOOD.
PRINTS; PR00010; EGFBLOOD.
PRINTS; PR00010; EGFBLOOD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00181; EGF; 2.
SMART; SM00179; EGF CA; 1.
SMART; SM00069; GLA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 36.4 Matches 16; Conservative
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GO; GO:0004295;
GO; GO:0006508;
InterPro; IPR000
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SEQUENCE
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Q99L32
                  RUCK RUCK WW FFF CS
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REPUBLIE-98-98-39 FUNDAMED 978-36-72;

REPUBLIE-98-98-39-31;

"Cloning and recombinant expression of mouse coagulation factor X.";

"Thromb. Res. 95-33-41|103-80].

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.

DR MED, M21-103-107;

RESP; PO0742; INTA.

DR MGD; MG1:103-107; FIO.

GO; GO:00055-0; C:extrachromeomal DNA; IEA.

MGD; MG1:103-107; FIO.

GO; GO:00055-0; F:calcium ion binding; IEA.

GO; GO:00058-0; F:calcium ion binding; IEA.

GO; GO:00042-0; F:calcium ion binding; IEA.

BR GO; GO:00042-0; F:calcium ion binding; IEA.

GO; GO:00042-0; F:calcium ion binding; IEA.

RICE-Pro; IPRO01-2-1 GFG-1-1.

RICE-Pro; IPRO01-2-1 GFG-1
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            054740;

01-UNN-1998 (TEMBLrel. 06, Last sequence update)

01-UNN-1998 (TEMBLrel. 06, Last sequence update)

01-OTT-2003 (TEMBLrel. 25, Last annotation update)

Coagulation factor X precursor (EC 3.4.21.6).

FIO OR FAIO.

Mus musculus (Mouse)

Plasmid pBluescript.

PLARATYOCE; Metazoa: Chordata; Craniata; Vortebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 40.9%; Pred. No. 4e-07;
Matches 18; Conservative 9; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 ANTFMEELKPASLERECREELCDFEEAREIFITREATLEFWTAY 83
                                                                                                                           Strausberg R.;
Submitted (UUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BO55118 AAH53182.1; -.
Hypothetical protein.
SEQUENCE 434 AA; 48516 MW; B47BD7947CF9D9C9 CRC64;
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
MEDLINE=98454993; PubMed=9783672;
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SMART; SM00069; GLA; 1.
SWART; SW000009; Tryp SPc; 1.
PROSITE; PS00010; ASK HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                             SEQUENCE FROM N.A
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                                                                                                     rissum=Kidney;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
PROSITE; PSO0022; EGF_1; 1.

PROSITE; PSO1186; EGF_CA; 1.

PROSITE; PSO1187; PGF_CA; 1.

PROSITE; PSO0011; GLU_CARBOXYLATION, 1.

PROSITE; PSO0134; TRYPSIN DOM; 1.

PROSITE; PSO0135; TRYPSIN HIS; 1.

PROSITE; PSO0135; TRYPSIN HIS; 1.

PROSITE; PSO0135; TRYPSIN HIS; 1.

PROFILE; PSO0135; TRYPSIN SER; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 ANSFFEEFKKGNLERECMEEICSYEEVREIFEDDEKTKEYWTKY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

EMBL; BC003877; AAH03877.1; --

HSSP; P00742; 1XKA.
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| RESOFS | VOLV42; IAAA. |
| RESOFS | VOLV42; IAAA. |
| RGD; MGI:103107; FIO. |
| RGD; MGI:103107; FIO. |
| RGD; GG:00005576; C:extracellular; IEA. |
| GG:00005505; F:calcium ion binding; IEA. |
| RGD; GG:00004263; F:calcium ion binding; IEA. |
| RICEPTO; IPR000152; Asx hydroxyl S. |
| RICEPTO; IPR000181; EGF _ II. |
| RICEPTO; IPR00181; EGF _ II. |
| RICEPTO; IPR001849; EGF _ II. |
| RESOFO; IPR001254; Poptidase _ SIA. |
| RESOFO; IPR001254; Poptidase _ SIA. |
| RESOFO; IPR00100; EGFELOOD. |
| REMART; SM00100; EGFELOOD. |
| REMART; SM00120; EGF _ II. |
| RESOFORE; PS01186; EGF _ II. |
| RESOFORE | II. |

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COAGULATION FACTOR X.
; CF702DE5EF9D97AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q99L32;
01-UUN-2001 (TrEMBLrel, 17, Created)
01-UUN-2001 (TrEMBLrel, 17, Last sequence update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
Coagulation factor X.
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47.0%; Score 93; DB 11; Length 481;
Best Local Similarity 36.4%; Pred. No. 4.5e-07;
Matches 16; Conservative 9; Mismatches 19; Indels
PROSITE; PS00011; GLU CAREOXYLATION; 1.
PROSITE; PS50240; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN HIS; 1.
PROSITE; PS00135; TRYPSIN ESE; 1.
EGF-like domain; Hydrolase; Protease; Serine protease.
SEQUENCE 481 AA; 54004 MW; BD88E96C8A0B7E7F CRC64;
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Search completed: March 1, 2004, 10:02:51 Job time: 40.5 secs

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Appli 52 70178 54 Appli 1, Appli 1, Appli 2, Appli 3, Appli 4, Appli 4, Appli 6, Appli 6, Appli 7, Appli 7, Appli 8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 8, Appli 9, Appli

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Sequence 2,
Sequence 2,
Sequence 2,
Sequence 3,
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Sequence 5
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Patent No. 6017882
GENERAL INFORMATION:
APPLICANT: Nolsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/00201
CURRENT FILING DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
LENGTH: 44
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Best Local Similarity 100.0%; Pred. No. 1.4e-23;
Matches 44; Conservative 0; Mismatches 0;
US-08-955-636-35
US-10-182-263-6
US-0178-2
US-08-229-280-5
US-09-065-872-1
US-09-667-570A-1
US-09-667-570A-2
US-08-955-636-2
US-08-955-636-2
US-08-330-978-2
US-08-347-07-2
US-08-474-042-2
US-08-474-042-2
US-08-474-042-2
US-08-484-558-2
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| Sequence 2.263.26
| Patent No. 6630138
| GENERAL INFORMATION
| APPLICANT: Gerlitz, Bruce E
| APPLICANT: Grimell, Brian W
| TILE OF INVENTION: PROTEIN C DERIVATIVES
| FILE REPERENCE: X-1361|
| CURRENT FILING DATE: 2002-07-22
| CURRENT FILING DATE: 2002-07-22
| PRIOR PILING DATE: 2002-011
| PRIOR PILING DATE: 2002-02-11
| PRIOR PILING DATE: 2000-03-14
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: Patentin version 3.1
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ORGANISM: Homo sapiens
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Sequence 24, Appl
                                                                                                                                    1, 2004, 10:03:28 ; Search time 16.5 Seconds (without alignments) 137.669 Million cell updates/sec
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Sequence 1,
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Patent No. 52
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Sequence 2(
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Sequence 25
Sequence 2,
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/cgm2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-10-182-263-3
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US-10-182-263-2
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       77.3%; Pred. No. 9.3e-22; rative 0; Mismatches 10;
       Best Local Similarity 77.3%
Matches 34; Conservative
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NAME/KEY: MOD RES
LOCATION: (0) ... ((
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US-08-955-636-1
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LENGTH: 44
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                                                                                                                                     Query Match 88.9%; Score 176; DB 4; Length 419; Best Local Similarity 77.3%; Pred. No. 9.3e-22; Matches 34; Conservative 0; Mismatches 10; Indels
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88.9%; Score 176; DB 4; Length 41

Best Local Similarity 77.3%; Pred. No. 9.3e-22;

Matches 34; Conservative 0; Mismatches 10; Indels
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APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Grimell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR PILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
SEQ ID NO 6
TYPE: PRT
COGGANISM: Homo sapiens
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APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grinnell, Brian W
TITLE CO INVENTION: PROTEIN C DERIVATIVES
FILE REPERBACE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR PILING DATE: 2002-02-11
PRIOR PILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENT NOS: 12
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Patent No. 6630138
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Patent No. 6630138
                                        TYPE: PRT;
CRGANISM: Homo sapiens
US-10-182-263-3
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ORGANISM: Homo sapiens
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SEQ ID NO 3
LENGTH: 419
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Sequence 1, Application US/08955636A; Patent No. 6017882; GENERAL INFORMATION: APPLICANT: Nelsestuen, Gary; TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT; TITLE OF INVENTION: POLYPEPTIDES; FILE REFERENCE: 09531/002011; CURRENT FILING DATE: 1997-10-23; NUMBER OF SEQ ID NOS: 35; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 1500 No. 1000 No. 10
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Sequence 20, Application US/08955636A

Patent No. 6017882

GENERAL INFORMATION:
APPLICANT: Nelsestuen, Gary
TITLE OF INVENTION: MODIFIED VITAMIN K-DEPENDENT
TITLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/002001
CURRENT APPLICATION NUMBER: US/08/955,636A

CURRENT FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FASTSEQ for Windows Version 3.0
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Best Local Similarity 97.7%; Pred. No. 3.3e-22;
Matches 43; Conservative 0; Mismatches 1
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ORGANISM: Homo sapiens
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RESULT 10
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LOCATION: (0) ...(0)
OTHER INFORMATION: Xaa=gamma carboxyglutamic acid or glutamic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.9%; Score 172; DB 3; Length 44; Best Local Similarity 97.7%; Pred. No. 3.3e-22; Matches 43; Conservative 0; Mismatches 1; Indels
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Patent No. 5847085
GENERAL INFORMATION:
APPLICANT: CHARLES T. ESMON AND MIKHALL D. SMIRNOV
TITLE OF INVENTION: Modified Protein C
NUMBER OF SEQUENCES;
CORRESPONDENCE ADDRESS;
ADDRESSEE: Patrea L. Pabet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nelsestuen, Gary
ITLLE OF INVENTION: MODIFIED UITAMIN K-DEPENDENT
ITLLE OF INVENTION: POLYPEPTIDES
FILE REFERENCE: 09531/00201
CURRENT APPLICATION NUMBER: US/08/955,636A
CURRENT PILIMG DATE: 1997-10-23
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 44
                  guence 21, Application US/08955636A
itent No. 6017882
SNERAL INPORMATION:
                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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18-955-636-21
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GENERAL INFORMATION:
APPLICANT: Griffin, John H.
APPLICANT: Mesters, Rolf M.
TITLE OF INVENTION: Serie Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "partial sequence of human protein C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 86.9%; Score 172; DB 2; Length 45; 1. Similarity 95.5%; Pred. No. 3.3e-22; 42; Conservative 2; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Office of Patent Counsel, The Scripps
ADDRESSEE: Research Institute
STREET: 10666 No. 5679639th Torrey Pines Road, TPC 8
                                                                                                                                                                                                               COUNTRIES READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYRE:
FLODDY disk
COMPUTER: IEM PC compatible
CORRENT TYRE:
FCLODG/MS-DOS
SOFTWARE:
FCLOMG/MS-DOS
SOFTWARE:
FRIEND DATA:
APPLICATION NUMBER:
CLASSIFICATION:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
BEGOURNER:
TELEFONE:
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OTHER INFORMATION: /note="where Kaa means gamma
OTHER INFORMATION: carboxylghutamic acid"
STREET: 2800 One Atlantic Center, 1201 West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-295-411-1
; Sequence 1, Application US/08295411
; Patent No. 5679639
                                               Peachtree Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
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APPLICANT: Griffin, John H.
APPLICANT: Mesters Rolf M.
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.9%; Score 172; DB 1; Length 419; 75.0%; Pred, No. 4.5e-21; tive 2; Mismatches 9; Indels
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ADDRESSEE: Research Institute
STREET: 10666 No. 5968751th Torrey Pines Road, TPC 8
STREET: J051a
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM FOCOMDATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PAECHLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/295,411
FILING DATE: 22-ANG-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
CLASSIFICATION: 530
CLASSIFICATION: 530
FILING DATE: 18-NOV-1991
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OTHER INFORMATION: /note= "Protein C Light Chain"
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LOCATION: 170..419
OTHER INFORMATION: /note= "Protein C Heavy Chain"
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                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Fiting, Thomas
REGISTRATION UNBER: 34,163
REFERNE/DOCKET NUMBER: 34,163
REFERNE/DOCKET NUMBER: 34,163
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08955471 Patent No. 5968751
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Matches 33; Conservative
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COMPUTER READABLE FORM:
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LOCATION: 158..169
OTHER INFORMATION: /
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US-08-955-471-1
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Sequence 3, Application US/09667570A;
Sequence 3, Application US/09667570A;
Parent NO. 6436337;
GENERAL INFORMATION:
APPLICANT: Baker, Jeffrey C;
APPLICANT: Carlson, Andrew D;
APPLICANT: Rhaling Theodore A;
TITLE OF INVENTION: Improved Methods for Processing Activated Protein C;
TITLE REFERENCE: X-11796A;
CURRENT APPLICATION NUMBER: US/09/667,570A;
CURRENT FILING DATE: 2000-09-21;
FRIOR APPLICATION NUMBER: 60/045,255;
FRIOR APPLICATION NUMBER: 60/045,255;
NUMBER OF SEQ ID NOS: 3;
SOFFWARE: Patentin version 3.1
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OTHER INFORMATION: /note= "Protein C Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; IOCATION: 170.419
OTHER INFORMATION: /note= "Protein C Heavy Chain'
US-08-955-471-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation
OTHER INFORMATION: Peptide"
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/955,471
FILIG DATE:
                                                                                                                                                                                                                                                                                                                                       NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERNCE/DOCKET NUMBER: TSRI263.0C1
TELECOMNUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/295,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 419 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CAGANISM: Homo sapiens
US-09-667-570A-3
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                                                                                                                                                                                     CLASSIFICATION:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Garner, Ian
APPLICANT: Cottingham, Ian R.
APPLICANT: Temperley, Simon M.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Prunkard, Donna E.
ITLE OF INVENTION: ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: Region

LOCATION: 170..419

OTHER INFORWATION: /note= "Protein C Heavy Chain"

PCT-US92-10242-1
                                                                                                                                                                                                                                                                                                                                                                                         /note= "Protein C Light Chain"
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Region
LOCATION: 158..169
OTHER INFORMATION: /note= "Protein C Activation
OTHER INFORMATION: Peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.9%; Score 172; DB 5; 75.0%; Pred. No. 4.5e-21; tive 2; Mismatches 9
                NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

RETERENCE/DOCKET NUMBER: 3CR0472P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
TELEPHONE: 619-554-6312
INFORMATION FOR SEQ ID NO: 1:
ENGRATION FOR SEQ ID NO: 1:
ENGRATION FOR SEQ ID NO: 1:
CAPPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: REGION
LOCATION: 1..157
OTHER INFORMATION: /note= "Protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08756506
Patent No. 5905185
GENERAL INFORMATION:
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NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.0
Matches 33, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-08-756-506-2
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APPLICANT: Mesters, Rolf
TITLE OF INVENTION: Serine Protease-Derived Polypeptides and
TITLE OF INVENTION: Anti-Peptide Antibodies, Systems and Therapeutic Methods
TITLE OF INVENTION: for Inhibiting Coagulation
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: ADDRESSE: Office of Patent Counsel, The Scripps
ADDRESSE: Research Institute
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
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                                                           Gaps
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             Score 172; DB 4; Length 419;
Pred. No. 4.5e-21;
2; Mismatches 9; Indels
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                                                                                            1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                       1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10242
FILING DATE: 19921118
                                                                                                                                                                                                                                        Sequence 1, Application US/10182263
Felent No. 6630138
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gorlitz, Bryan E
APPLICANT: Gorlinel, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182, 263
CURRENT APPLICATION NUMBER: 60/181946
PRIOR APPLICATION NUMBER: 60/181946
PRIOR PILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3:1
LENGTH: 419
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/793,989
FILING DATE: 18-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9210242 GENERAL INFORMATION:
      Query Match
Best Local Similarity 75.0%;
Matches 33; Conservative
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Matches 33; Conservative
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ORGANISM: Homo sapiens
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAX: 206-442-6678
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE FRARACTERISTICS:
LENGTH: 460 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: TYPE: Drotcein
US-08-756-506-2
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Query Match 86.9%; Score 172; DB 2; Length 460; Best Local Similarity 75.0%; Pred. No. Se-21; Matches 33; Conservative 2; Mismatches 9; Indels 0; Gaps

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Search completed: March 1, 2004, 10:12:20 Job time : 17.5 secs



232, App 244, Appl 244, Appl 218, Appl 21, Appl

Sequence 3 Sequence Sequence 1

Sequence

Sequence 1 Sequence 3 Sequence 1

Sequence Sequence Sequence

Appl Appl Appl App

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Sequence Sequence Sequence

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Sequence

Sequence Sequence

Sequence 43, Sequence 312,

Sequence

Sequence

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1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
US-10-298-330-2
US-10-360-101-232
US-10-348-504-44
US-10-298-504-44
US-10-298-330-18
US-10-383-898-1
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88.9%; Score 176; DB 14;
Best Local Similarity 77.3%; Pred. No. 5.6e-21;
Matches 34; Conservative 0; Mismatches 10;
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US-10-188-495-40
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Publication No. US20030022354A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bruce E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRÊNT APPLICATION NUMBER: US/10/182, Z63
CURRENT PILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181948
PRIOR PILING DATE: 2002-02-11
PRIOR PILING DATE: 2002-01-11
PRIOR PILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 3: SEQ ID NOS: 12
SEQ ID NO 3: SEQ ID NOS: 12
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Publication No. US20030022354A1
GENERAL INFORMATION:
   TYPE: PRT
ORGANISM: Homo sapiens
   10-182-263-3
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US-10-182-263-4
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US07_BWW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-10-182-263-5
US-10-168-407-3
US-10-298-330-1
US-09-978-917A-4
US-10-168-4077-1
US-10-168-407-1
US-09-978-917A-2
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US-10-168-407-6
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Maximum Match 100%
Listing first 45 summaries
                                                                              protein search, using sw model
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seq length: 200000000
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Perfect score:
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1 LOCATION: 6, 7, 14, 16, 19, 20, 25, 26, 29

2 OTHER INFORMATION: Xaa = gamma carboxyglutamic or glutamic acid

US-10-298-330-1
                                                                                                                                                                                                  Length 419;
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Pred. No. 5.6e-21;
0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                             1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
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| Publication No. US20030100506A1
| GENERAL INFORMATION: W20030100506A1
| APPLICATION No. US20030100506A1
| TITLE OF INVENTION: Modified Vitamin K-Dependent TITLE OF INVENTION: POLYPEPtides
| CURRENT APPLICATION NUMBER: US/10/298,330
| CURRENT FILING DATE: 2000-12-18
| PRIOR PELICATION NUMBER: 09/407,591
| PRIOR PELICATION NUMBER: 09/402,29
| PRIOR PELICATION NUMBER: 08/955,636
| PRIOR FILING DATE: 1999-04-29
| PRIOR FILING DATE: 1997-10-23
| NUMBER OF SEQ ID NOS: 27
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                             Score 176; DB 15;
Pred. No. 5.6e-21;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT FILICATION NUMBER: US/10/168,407
CURRENT FILITG DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
                      ; SOFTWARE: Patentin version 3.1; SEQ ID NO 3; LENGTH: 419; TYPE: PRT; TYPE: PRT; ORGANISM: Homo sapiens
                                                                                                                                                                                        Query Match
Best Local Similarity 77.3%;
Matches 34; Conservative
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Best Local Similarity 77.3%;
Matches 34; Conservative (
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US-10-168-407-4
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Pred. No. 5.6e-21;
0; Mismatches 10; Indels (
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ilarity 77.3%; Pred. No. 5.6e-21;
Conservative 0; Mismatches 10; Indels
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APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
APPLICANT: Gerinnell, Brian W
ITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181946
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-03-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
LENGTARE: PatentIn version 3.1
LENGTH: 419
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Publication No. US20030022354A1
Publication No. US20030022354A1
APPLICANT: Gerlitz, Bruce E
APPLICANT: Gerlitz, Bryan E
TITLE OF INVENTION: PROTEIN US/10/182, 263
CURRENT APPLICATION WUMBER: US/10/182, 263
CURRENT APPLICATION NUMBER: 60/181948
PRIOR APPLICATION NUMBER: 60/181948
PRIOR FILING DATE: 2002-02-11
PRIOR FILING DATE: 2002-03-14
PRIOR FILING DATE: 2000-03-14
SPRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: RetentIn Version 3.1
SEQ ID NO S:
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Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: GETLIC, Bruce E
APPLICANT: OFF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
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Best Local Similarity 77.3%;
Matches 34; Conservative
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-182-263-5
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TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REPERENCE: 021948310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 2.6e-20;
2; Mismatches 9; Indels
Query Match 86.9%; Score 172; DB 14; Length 44; Best Local Similarity 95.5%; Pred. No. 2.2e-21; Matches 42; Conservative 2; Mismatches 0; Indels
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Pred. No. 2.6e-20;
2; Mismatches 9; Indels
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APPLICANT: Gerlitz, Bryan E
APPLICANT: Jones, Bryan E
APPLICANT: Grinnell, Brian W
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/18919
PRIOR PLING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
PRIOR FILING DATE: 2000-03-14
STOR APPLICATION NUMBER: 60/18919
PRIOR FILING DATE: 2000-03-14
STOR APPLICATION NUMBER: 60/18919
PRIOR FILING DATE: 2000-03-14
STOR APPLICATION NUMBER: 60/18919
PRIOR FILING DATE: 2000-03-14
STOR DE SEQ ID NOS: 12
SOFTWARE: PATENT NOS: 12
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                            Sequence 4, Application US/09978917A Publication No. US20030027299A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10182263; Publication No. US20030022354A1; GENERAL INFORMATION:
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1 Similarity 75.0%;
33; Conservative
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Best Local Similarity 75.0%;
Matches 33; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-182-263-1
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Matches 33; Conserv
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TYPE: PRT
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US-10-168-407-1
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TITLE OF INVENTION: Protein C or activated protein C-like molecules
FILE REFERENCE: 0219us310 - protein C
CURRENT APPLICATION NUMBER: US/09/978,917A
CURRENT FILING DATE: 2001-10-17
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
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GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Publication No. US20300223541
GENERAL INFORMATION:
APPLICANT: Geriltz, Bruce E
APPLICANT: Gories, Bryan B
APPLICANT: Grinnell, Brian W
ITILE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13611
CURRENT APPLICATION NUMBER: US/10/182,263
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: 60/181946
PRIOR PLING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: 60/18199
PRIOR FILING DATE: 2000-03-14
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Matches 33; Conservative
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US-10-168-407-1
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ORGANISM: Homo sapiens
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LOCATION: (43)...(461)
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NAME/KEY: SIGNAL
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TYPE: PRT
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86.9%; Score 172; DB 14; Length 461;
Best Local Similarity 75.0%; Pred. No. 2.9e-20;
Matches 33; Conservative 2; Mismatches 9; Indels
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86.9%; Score 172; DB 15; Length 461;

Best Local Similarity 75.0%; Pred. No. 2.9e-20;

Matches 33; Conservative 2; Mismatches 9; Indels (
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84.8%; Score 168; DB.14; Length 419;
Best Local Similarity 75.0%; Pred. No. 1.2e-19;
Matches 33; Conservative 0; Mismatches 11; Indels (
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; Sequence 6, Application US/10182263
; Publication No. US20030022354A1
; GENERAL INFORMATION:
APPLICANT: Gerlitz, Bruce E
; APPLICANT: Gerlitz, Bruce E
; APPLICANT: Grinnell, Bruce E
; APPLICANT: WINNER: US/10/182,263
FILE REFRENCE: X-13611
; CURRENT APPLICATION NUMBER: G0/181948
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: 60/189199
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PATENTIN version 3.1
; SEQ ID NO 6
; LENGTH. A. A.
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| Publication No. US20030207435A1
| GENERAL INFORMATION: US20030207435A1
| APPLICANT: Gerlitz, Bruce E
| APPLICANT: Gones, Bryan E
| TILLE OF INVENION: PROTEIN C DERIVATIVES
| FILE REFERENCE: X-13610
| CURRENT APPLICATION NUMBER: US/10/168,407
| CURRENT FILING DATE: 2002-11-04
| NUMBER OF SEQ ID NOS: 12
| SOFTWARE: Patentin version 3.1
| SOFTWARE: PROTEIN OF SEQ ID NOS: 12
| SOFTWARE: PROTEIN OF SEQ ID NOS: 12
| SOFTWARE: PROTEIN OF SEQ ID NOS: 13
| SOFTWARE: PROTEIN OF SEQ ID NOS: 14
| SOFTWARE: PROTEIN OF SEQ ID NOS: 15

NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 461
                                                                                                                                                                          TYPE: PRT
CORGANISM: Homo sapiens
US-10-182-263-2
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CORGANISM: Homo sapiens
US-10-182-263-6
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US-10-168-407-2
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1 ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                   1 ANSFLEBLROGSLERECIBBICDFBEAKEIFEDVDDTLAFWSKH 44
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Publication No. US20030207435A1
GENERAL INPORMATION:
APPLICANT: Gerlitz, Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REFERENCE: X-13610
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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Sequence 6, Application US/10168407
Publication No. US20030207435A1
GENERAL INFORMATION:
APPLICANT: GETALIZ. Bruce E
APPLICANT: Jones, Bryan E
TITLE OF INVENTION: PROTEIN C DERIVATIVES
FILE REPERBENCE: X-13310
CURRENT APPLICATION NUMBER: US/10/168,407
CURRENT FILING DATE: 2002-11-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 6.
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ORGANISM: Homo sapiens
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US-10-168-407-6
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

March Run on:

1, 2004, 09:54:37; Search time 50 Seconds (without alignments) 248.642 Million cell updates/sec

SEQ1-4SUBS 197 Title: Perfect

score:

1 ANSFLXXLRqgSLXRXCIXX.........XXAXXIFedVDDTLAFWSKH 44 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters: 1586107 segs, 282547505 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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geneseqp2003as; *
geneseqp2003bs; *
geneseqp20048; * A_Geneseq_29Jan04:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	18	Aab826	Aab826	Aae086	Aay183	Aab826	Aab8267	Aae086	Aae086	m	Aay18298	7182	7182	y183	α	6799	Adb71159	0799	Aay183	Aay183	b 3641	42009	W757	5799	Adb711	
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SUMMARIES			00	77	78	30	01	9/9	75	28	27	629	298	66	97	02	949	46	S O	20	309	03	402	94	710	47	S S	
SUM			AAY183	AAB826		m			N	m	36			AAY182		AAY183	ABB799	\mathbf{a}	_	$\boldsymbol{\sigma}$		7183		95009	10	S.	3711	
		A	AA	AA	AAB8	AAE0	AAY1	AAB8	AAB8	AAE0	AAEO	AAE0	AAY1	Ā	AAY1	A	ABI	ABB7	AD	ABB7	AAY1	AAY1	AAB3	ADD5	AAW7	ABB7	ADB	
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æ	Query	Mat	90	8	90	8	8	88	88	88	88	88	87	96	82	82	82	83	83	82	81	81	8	8	8	81	81	
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. 60	9	275	Aab82673 Wild-type	89	5897 Human	1898 Human	Human	Aae08625 Human mat	Aau99005 Human Pro	Aau99006 Human Pro	9 Human	. Aau99018 Human Pro	Aau99026 Human Pro	Aau99037 Human Pro	Aau99049 Human Pro	Aau99063 Human Pro	Aau99072 Human Pro	Aau99083 Human Pro	Aau99084 Human Pro
AAY56803	AAR35760	AAW72753	AAB82673	AAB36896		AAB36898	AAB36894	AAE08625	AAU99005	AAU99006	AAU99008	AAU99018	AAU99026	AAU99037	AAU99049	AAU99063	AAU99072	AAU99083	AAU99084
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9	9	φ	9	9	9	Q	v	φ	9	φ	9	ø	160	φ	ø	160	Θ	φ	160
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

GLA domain; mutein; vitamin K-dependent protein; clotting disorder; Modified GLA domain of vitamin K-dependent protein. AAY18300 standard; peptide; 44 AA. (first entry) 17-AUG-1999 AAY18300; therapy. RESULT 1

Location/Qualifiers Key Misc-difference Homo sapiens. Synthetic. X B X & E X S S X E E E E

 .44 /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid" WO9920767-A1 29-APR-1999.

97US-00955636. (MINU) UNIV MINNESOTA Nelsestuen GL; 23-OCT-1997;

98WO-US022152.

20-OCT-1998;

WPI; 1999-288309/24.

Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.

Claim 9, Page 79, 86pp, English.

This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein

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Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerlitz BE,
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/note= "activation peptide; removal activates the 2-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 .157
/hote= "cleavage makes a 2-chain inactive precursor (155-
amino acid light chain attached via a disulfide bond to a
262-amino acid heavy chain)"
                                                                                                                                                                                                                                                                                                                                                                                                Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy; mutant; mutein.
                                                                                           Gaps
                                                                                           ..
                                                    Length 44;
                                                                                         0; Indels
                                                                                                                          1 ANSFLXXLRQGSLXRXCIXXICDFXXAXXIFEDVDDTLAFWSKH 44
                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                  Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Gln in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "His in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Asn in wild-type protein"
                                                  90.9%; Score 179; DB 2; I larity 100.0%; Pred. No. 2.3e-22; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .45
/note= "Gla domain"
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                                                                                                                                                                                                                                                 AAB82677 standard; protein; 419
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                                                                      Local Similarity
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Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Cleavage-site
                   Sequence 44 AA;
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Synthetic.
                                                                                                                                                                                                                                                                                                                             15-0CT-2001
                                                                                         44;
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                                                      Query Match
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Domain
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Matches
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AAB82677
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The present sequence is that of a claimed human protein C derivative in which His at position 10 of the marure wild-type protein C sequence (see AABS273) is substituted with Glu, Ser at position 11 with Glu, at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. It is an example of protein C derivatives of the invention thave at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives are useful for treating coronary syndromes and disease states predisposing to cromary syndromes and disease states predisposing to thrombosis (e.g. mycocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in coronary catherer), protein C deficiency, acute arterial thrombotic occlusion, proteins of active arterial thrombotic coclusion, thrombotic disorders in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders with genetically predisposed prothrombotic disorders with genetically predisposed prothrombotic disorders with genetically predisposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating, e.g., myocardial thrombotic disorders, acute arterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANSFLEELROGSLERECIEFICDFERAKEIFEDVDDTLAFWSKH 44
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                                                               note= "Leu in wild-type protein"
note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human protein C derivative for treat
infarction, unstable angina, sepsis, throm
thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                 /note= "N-glycosylated"
331. .345
356. .384
                                                                                                                                                                                                                                                                         'note= "N-glycosylated"
                                                                                                                                                                                             note= "N-glycosylated'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-2000; 2000US-0179801P.
14-MAR-2000; 2000US-0189197P.
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                                                                                                                 196. .212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-496919/54.
N-PSDB; AAH26365.
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                                     Misc-difference
                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157193-A2
                                                                                                                                                            Modified-site
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15-OCT-2001

Modified-site Modified-site

Domain

Homo sapiens Synthetic.

Modified-site

Modified-site Modified-site Modified-site Modified-site

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The present sequence is that of a claimed human protein C derivative in which His at position 10 of the wild-type protein C sequence (see AABS2673) is substituted with Glu, Ser at position 13 with Gly, Glu at position 33 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid derivatives of the invention that have an example of protein C derivatives of the wild-type are sistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. While retaining the biological activity of the wild-type protein. The protein of derivatives are useful for treating methods is claimed. The protein of derivatives are useful for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angula), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal thrombotic disorders (in combination with an anti-platelet agent to by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular graffs. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
                                                                                                                                                                                                                                                                                                               Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; protein C derivative; anticoagulation activity; thrombosis; serpin inactivation; acute coronary syndrome; myocardial infarction; vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn; transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.9%; Score 179; DB 4; Length 419; 79.5%; Pred. No. 2.5e-21; ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                                                                                                                                                                                                                                                                                                                          infarction, unstable angina, sepsis, throm
thrombotic occlusion, and thromboembolism.
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 56-57; 63pp; English
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                                                               19-JAN-2001; 2001WO-US000020.
                                                                                                             02-FEB-2000; 2000US-0179801P.
14-MAR-2000; 2000US-0189197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 79.55
Matches 35; Conservative
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                                                                                                                                                                         (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                      WPI; 2001-496919/54.
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                     09-AUG-2001
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/note= "cleavage makes a 2-chain inactive precursor (155-

amino acid light chain attached via a disulfide bond to a

262-amino acid heavy chain)"

158. .169

/note= "activation peptide; removal activates the 2-chain
                                                                                              Protein C; human; coronary syndrome; thrombosis; angina; myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy; mutant; mutein.
                                                     Human protein C derivative (H10Q/S11G/Q32E/N33D/L194S/T254S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "His in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Asn in wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "Thr in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Gln in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "thrombin cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                    note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "gamma-carboxylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      'note= "Gla domain"
            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331. .345
356. .384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196. .212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zymogen"
                                                                                                                                                                                                                                                                                                                             .45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
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Modified-site Modified-site

Disulfide-bond Disulfide-bond

WO200157193-A2

Disulfide-bond

Cleavage-site

Peptide

Cleavage-site

Modified-site

Modified-site Modified-site

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Gaps

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seq1-4subs.rag

WO200159084-A1

16-AUG-2001

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Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared disorder by decreasing or increasing of the containing of the containing of the containing of the containing of the modification. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein C; human, coronary syndrome; thrombosis; angina; myccardial infarction; vascular occlusive disorder; hypercoagulation; sepsis; protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLXXLREGSLXRXCIXXICDFXXAKXIFBDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein C derivative (S11G/Q32E/N33D/L194S/T254S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Ser in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11arity 97.7%; Pred. No. 7.2e-22; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ...45
'note= "Gla domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB82676 standard; protein; 419 AA
                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 82; 86pp; English
                                                                                                            98WO-US022152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                     WPI; 1999-288309/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                          Welsestuen GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                            20-OCT-1998;
                                                                 29-APR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB82676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ношо
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AAB82676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human protein C derivatives and nucleic acid
molecules encoding such derivatives. These derivatives have increased
anticoappllation activity, resistance to serpin inactivation and increased
sensitivity to thrombin activation compared to wild type protein C, and
retains the biological activity of the wild type human protein C, and
certains the biological activity of the wild type human protein C, and
certains the biological activity of the wild type human protein C, and
certains the biological activity of the wild type human protein C. and
certains the biological activity of the wild type human protein C. Protein
certains the biological activity of the wild type human for the
certains are useful in the manufacture of a medicament for the
certains and disease states predisposing to thrombosis, vascular
certains and hypercoagulable states e.g. disseminated
coclusions, tablassamena,
sickle cell disease, viral haemorrhagic fever and haemolytic uremic
syndrome; sepsis in combination with bacterial permeability increasing
protein; thrombotic disorders in combination with an anti-platelet agent;
corin vascular graffs in combination with a thrombotic agent. Nucleic
corin wascular graffs in combination with a thrombotytic agent. Nucleic
corin wascular graffs in combination with a thrombotytic agent. Nucleic
corin molecules of the invention are useful for treating humans with
correspond to present sequence is human protein C derivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                        Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 179; DB 4; Length 419;
Pred. No. 2.5e-21;
0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANSFLEELROGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                      Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 50-51; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY18301 standard; peptide; 44
                                                                           02-FEB-2001; 2001WO-US001221.
                                                                                                                     11-FEB-2000; 2000US-0181948P.
                                                                                                                                          14-MAR-2000; 2000US-0189199P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 79.5%;
Matches 35; Conservative (
                                                                                                                                                                                                                                 Grinnell BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                  (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                         WPI; 2001-514662/56.
N-PSDB; AAD15228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
Synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1999
                                                                                                                                                                                                                                 Gerlitz BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY18301;
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Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "activation peptide; removal activates the 2-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a claimed human protein C derivative in which Ser at position 11 of the mature wild-type protein C sequence (see AABS2673) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, Leu at position 194 with Ser, and Thr at position 254 with Ser. It is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a 2-chain inactive precursor (155 attached via a disulfide bond to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute
                                                                                                                                                                                                                                                                               'note= "Gln in wild-type protein"
                                                                                                                                                                                                                                                                                                                                         "Asn in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Thr in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Leu in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "thrombin cleavage site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156. .157
/hocke= "cleavage makes a 2-ch
amino acid light chain attach
262-amino acid heavy chain)"
                                                                                                             note= "gamma-carboxylated"
                                                                                                                                                                 note= "gamma-carboxylated"
note= "gamma-carboxylated"
                                                   note= "gamma-carboxylated"
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                                                                                                                                                                                                                           note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 53-54; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-2001; 2001WO-US000020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02~FEB-2000; 2000US-0179801P
14-MAR-2000; 2000US-0189197P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331. 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196. .212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Ymogen"
                                                                                                                                                                                                                                                                                                                                               note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones BE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-496919/54.
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                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Disulfide-bond
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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Disulfide-bond
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                     Modified-site
                                                                                                                                   Modified-site
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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Peptide

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                for treating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular coclusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an antipathelet agent or by local delivery through an intracoronary catheter), protein C deficiency, acute arterial thrombotic occlusion, thrombotism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)
     The protein C derivatives are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myocardial infarction; vascular occlusive disorder; hypercoagulation; sepsis, protein C deficiency; occlusion; thromboembolism; stenosis; antibacterial; immunosuppressive; thrombolytic; cardiant; antianginal; anticoagulant; therapy; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                               Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein C; human; coronary syndrome; thrombosis; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein C derivative (S11G/Q32E/N33D/L194S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "Ser in wild-type protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Asn in wild-type protein"
                                                                                                                                                                                                                                                                                                                                                               88.3%; Score 174; DB 4;
77.3%; Pred. No. 1.7e-20;
iive 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "gamma-carboxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "gamma-carboxylated"
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recombinant DNA methods is claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers

    45
    note= "Gla domain"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.3
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 69
. 64
. 109
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                                                                                                                                                                                                                                                                                                             Sequence 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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Disulfide-bond
Disulfide-bond
Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB82675;
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Novel human protein C derivative for treating, e.g., myocardial infarction, unstable angina, sepsis, thrombotic disorders, acute arterial thrombotic occlusion, and thromboembolism.
                                                                                'note= "Leu in wild-type protein"
                                                            .69. .170
note= "thrombin cleavage site"
                                                                                                   note= "N-glycosylated"
                                                                                                                 /note= "N-glycosylated"
                                                                                                                              note= "N-glycosylated"
                                                                                                                                                                                                                                                                                              Claim 3; Page 52-53; 63pp; English.
                                                                                                                                                                                    19-JAN-2001; 2001WO-US000020,
                                                                                                                                                                                                02-FEB-2000; 2000US-0179801P.
14-MAR-2000; 2000US-0189197P.
                                                                                      196. .212
                                                      zymogen"
                                                                                                                                                                                                                    (ELIL ) LILLY & CO ELI
                                                                                                                                                                                                                                   Jones BE
                                                                                                                                                                                                                                               WPI; 2001-496919/54.
                                                                                                                                                                                                                                                      N-PSDB; AAH26363
Disulfide-bond
Disulfide-bond
Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 419 AA;
                                                                         Misc-difference
                                                                                     Disulfide-bond
Modified-site
                                                                                                                                    Disulfide-bond
Disulfide-bond
                                                                                                                                                        WO200157193-A2
                                                            Cleavage-site
                                                                                                                       Modified-site
                                                                                                                                                                      09-AUG-2001
                                                                                                                                                                                                                                  Gerlitz BE,
                                        Peptide
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The present sequence is that of a claimed human protein C derivative in which Ser at amino acid position 11 of the mature wild-type protein C sequence (see AAB8253) is substituted with Gly, Gln at position 32 with Glu, Asn at position 33 with Asp, and Leu at position 194 with Ser. The protein is an example of protein C derivatives of the invention that have at least 2 amino acid substitutions, but which have increased anticoagulant activity and resistance to inactivation by serpins compared with the wild-type protein, while retaining the biological activity of the wild-type protein. A method of producing the derivatives using recombinant DNA methods is claimed. The protein C derivatives using the creating coronary syndromes and disease states predisposing to thrombosis (e.g. myocardial infarction and unstable angina), vascular occlusive disorders and hypercoagulable states, sepsis (in combination with bactericidal permeability increasing protein or with tissue factor pathway inhibitor), thrombotic disorders (in combination with an antipercent C deficiency, acute arterial thrombotic occlusion, protein combination with an antipercent C deficiency, acute arterial thrombotic occlusion, protein combination with an antipercent C deficiency, acute arterial thrombotic occlusion, arterial arterial thrombotic occlusion. thromboembolism, or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts. Human patients with genetically predisposed prothrombotic disorders may be treated by gene therapy (all claimed)

88.3%; Score 174; DB 4; 77.3%; Pred: No. 1.7e-20; 0; Mismatches Local Similarity 77.3 les 34; Conservative Query Match

1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

ANSFLEELRHGSLERECIEBICDFEEAKEIFEDVDDTLAFWSKH 44

AAE08628 standard; protein; 419 AAE08628

01-NOV-2001 (first entry) AAE08628;

Human protein C derivative #2.

Human, protein C derivative; anticoagulation activity, thrombosis, serpin inactivation; acute coronary syndrome, myocardial infarction, vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn, transplantation, sickle cell disease, viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.

Homo sapiens

WO200159084-A1.

16-AUG-2001

02-FEB-2001; 2001WO-US001221

11-FEB-2000; 2000US-0181948P. 14-MAR-2000; 2000US-0189199P.

(ELIL) LILLY & CO ELI

Jones Grinnell Gerlitz BE,

BE;

WPI'; 2001-514662/56. N-PSDB; AAD15226.

Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.

Claim 4; Page 47-48; 59pp; English

The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased canticoagulation activity of the wild type protein C, and retains the biological activity of the wild type human protein C, and carturatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing sickle cell disease, viral haemorrhagic fever and nami-platelet agent; protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombocic occlusion; thrombotendism or stenosis in coronary, cerebral or periphefal arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with.

Second molecules of the invention are useful for treating humans with present sequence is human protein C derivative

Sequence 419 AA;

. 0 88.3%; Score 174; DB 4; Length 419; ilarity 77.3%; Pred. No. 1.7e-20; Conservative 0; Mismatches 10; Indels Query Match Best Local Similarity 34; Matches

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Gaps ; 0

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Gaps

1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44 à

1 ANSFLEELRHGSLERECIEFICDFEEAKEIFEDVDDTLAFWSKH 44 AAE08627 standard; protein; 419 AA Human protein C derivative #1. (first entry) Homo sapiens, 01-NOV-2001 AAE08627; AAE08627 RESULT

Human, protein C derivative; anticoagulation activity, thrombosis, serpin inactivation; acute coronary syndrome, myocardial infarction, vascular occlusive disorder; hypercoagulable state; angina; sepsis; disseminated intravascular coagulation; DIC; burn, transplantation; sickle cell disease; viral haemorrhagic fever; protein C deficiency; haemolytic uremic syndrome; acute arterial thrombotic occlusion; thromboembolism; prothrombotic disorder; gene therapy; thalassaemia.

WO200159084-A1 6-AUG-2001

02-FEB-2001; 2001WO-US001221.

11-FEB-2000; 2000US-0181948P. 14-MAR-2000; 2000US-0189199P.

(ELIL) LILLY & CO ELI

Jones BE; Grinnell BW, Gerlitz BE, WPI; 2001-514662/56 N-PSDB; AAD15225

Claim 3; Page 46-47; 59pp; English,

Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.

The invention relates to human protein C derivatives and nucleic acid molecules encoding such derivatives. These derivatives have increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C, and retains the biological activity of the wild type human protein C, and retains the biological activity of the wild type human protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute occupanty syndromes e.g. myocardial infarction and unstable angina; and disease states predisposing to thrombosis; vascular occupation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorrhagic fever and haemolytic uremic sickle cell disease, viral haemorrhagic fever and haemolytic uremic protein; thrombotic disorders in combination with bacterial permeability increasing protein; thrombotic disorders in combination with a nati-platelet agent; thrombotic manufacture arterial thrombotic occlusion.

Thrombotules of the invention are useful for treating humans with research examinated in human protein disorders by gene therapy. The present sequence is human protein C derivative

Sequence 419 AA;

Gaps ö 10; Indels 88.3%; Score 174; DB 4; 77.3%; Pred. No. 1.7e-20; iive 0; Mismatches 10; Query Match
Best Local Similarity 77.33
Matches 34, Conservative

1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44

1 ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH 44

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AAE08629 standard; protein; 419 AA.

AAE08629;

(first entry) 01-NOV-2001 Human protein C derivative #3.

Human, protein C derivative, anticoagulation activity, thrombosis, serpin inactivation, acute coronary syndrome, myocardial infarction, vascular occlusive disorder; hypercoagulable state, angina, sepsis) disseminated intravascular coagulation, DIC; burn; transplantation; sickle cell disease, viral haemorrhagic fever; protein C deficiency; haemolytic urem.c syndrome, acute arterial thrombotic occlusion, thromboembolism, prothrombotic disorder; gene therapy; thalassaemia.

Location/Qualifiers Misc-difference 10

/note= "Encoded by CAA"

WO200159084-A1

16-AUG-2001

02-FEB-2001; 2001WO-US001221

11~FEB-2000; 2000US-0181948P. 14-MAR-2000; 2000US-0189199P.

(ELIL) LILLY & CO ELI

Jones Grinnell BW, Gerlitz BE,

WPI; 2001-514662/56. N-PSDB; AAD15227.

Protein C derivative for treating acute coronary syndromes, vascular occlusive disorders, thrombotic disorders and sepsis, comprises substitutions at specified amino acid positions.

Claim 5; Page 48-49; 59pp; English.

The invention relates to human protein C derivatives and nucleic acid annicoagulation activity, resistance to serpin inactivation and increased anticoagulation activity, resistance to serpin inactivation and increased sensitivity to thrombin activation compared to wild type protein C, and retains the biological activity of the wild type human protein C. Protein C derivatives are useful in the manufacture of a medicament for the treatment of acute coronary syndromes e.g. myocardial infarction and unstable angina, and disease states predisposing to thrombosis, vascular occlusive disorders and hypercoagulable states e.g. disseminated intravascular coagulation (DIC), burns, transplantations, thalassaemia, sickle cell disease, viral haemorthagic fever and haemolytic uremic syndrome; sepsis in combination with bacterial permeability increasing syndrome, sepsis in combination with bacterial permeability increasing protein; thrombotic disorders in combination with an anti-platelet agent; protein C deficiency; acute arterial thrombotic occlusion, thromboembolism or stenosis in coronary, cerebral or peripheral arteries or in vascular grafts in combination with a thrombolytic agent. Nucleic acid molecules of the invention are useful for treating humans with genetically predisposed prothrombotic disorders by gene therapy. The present sequence is human protein C derivative

Sequence 419 AA;

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DB 4; 88.3%; Score 174; ω

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98WO-US022152.
                                                                                                                                                                                                                                            97US-00955636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.5%;
Matche's 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY18297 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                               (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                          WPI; 1999-288309/24.
                                                                                                                       Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 44 AA;
                                                                                                                                                                                                                                                                                    Nelsestuen GL;
                17-AUG-1999
                                                                                                                                                                                                                                            23-OCT-1997;
                                                                                         Нощо варіепв
                                                                                                                                                                                                                     20-0CT-1998;
                                                                                                                                                                            WO9920767-A1
                                                                                                                                                                                                 29-APR-1999
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                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY18297;
                                                                  therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the GLA domain results in a protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
              Gaps

    1. 44
    /note= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"

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                                                                                                                                                                                          domain; mutein; vitamin K-dependent protein; clotting disorder;
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77.3%; Pred. No. 1.7e-20;
tive 0; Mismatches 10; Indels
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                               1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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                                               ANSFLEELRHGSLERECIEEICDFEEAKEIFEDVDDTLAFWSKH
                                                                                                                                                                    Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 87.8%; Score 173; DB 2; Similarity 97.7%; Pred. No. 2.3e-21; 43; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                      AAY18298 standard; peptide; 44 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 78; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                               97US-00955636.
                                                                                                                                                                                                                                                                                                                                                          98WO-US022152.
                                                                                                                                                  (first entry)
Similarity 77.3 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   (MINU ) UNIV MINNESOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-288309/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Nelsestuen GL
                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         20-OCT-1998;
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                                                                                                                                                  17-AUG-1999
                                                                                                                                                                                                                                                                                                                                    29-APR-1999
                                                                                                                                                                                                                                       Synthetic.
                                                                                                                            AAY18298
Best Local
Matches 3
                                                                                                                                                                                                      therapy
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Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein which has enhanced membrane binding affinity as compared to the native protein

    44
    7ncte= "Xaa= gamma-carboxyglutamic acid, or glutamic acid"
acid"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                         GLA domain, mutein, vitamin K-dependent protein, clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain; mutein; vitamin K-dependent protein; clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a modified GLA (gamma-carboxyglutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANSFLXXLRESSLXRXCIXXICDFXXARXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 170; DB 2; L. Pred. No. 7.4e-21; 1; Mismatches 1;
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 78; 86pp; English
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Misc-difference 1. .44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy.
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AAY18299 standard; peptide; 44 AA

RESULT 12 AAY18299

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AAY18299

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This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared tio the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein C; Gla domain; human; blood clotting; anticoagulant; thrombolytic; antiarteriosclerotic; cardiant; antiaggregant; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New variant blood coagulation component, useful for manufacturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          medicament for treating or preventing coagulation disorders, e.g. thrombosis, comprises an anticoagulant activity in the protein Canticoagulant system of blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "wild-type His substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLROGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "wild-type Ser substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "wild-type Ser substituted
                                                                                                                                                                                                                                                                                                                                                                                        85.3%; Score 168; DB 2;
95.5%; Pred. No. 1.6e-20;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TACT-) TAC THROMBOSIS & COAGULATION AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein C mutated Gla domain QGN,
                                                                                                                                          Disclosure; Page 79; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB79949 standard; protein; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32-MAR-2001; 2001US-0272466P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002; 2002WO-SE000363
                                                                                                                                                                                                                                                                                                                                                                                                                              42; Conservative
                                                WPI; 1999-288309/24.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-713449/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Misc-difference
                                                                                                                                                                                                                                                                                                                                                     Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
            Nelsestuen GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200270681-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB79949;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
          #X#X##X8X000000000X8
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                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a modified GLA (gamma-carboxyglutamic acid) domain. The invention relates to a vitamin K-dependent polypeptide comprising a modified GLA domain containing an amino acid substitution which enhances membrane binding of the modified polypeptide as compared to the native polypeptide. The polypeptide is used to treat a clotting disorder by decreasing or increasing clot formation. Modification of the affinity as compared to the native protein which has enhanced membrane binding affinity as compared to the native protein
                                                                                                                                                                                                                                                                                                                     Vitamin K-dependent polypeptide with modified gamma-carboxyglutamic acid domain, useful for treating clotting disorders.
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps

    44
/note= "Xaa= gamma-carboxyglutamic acid, or glutamic

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLA domain; mutein; vitamin K-dependent protein; clotting disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 44;
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1 Similarity 95.5%; Pred. No. 1.6e-20;
42; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANSFLXXLRHSSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified GLA domain of vitamin K-dependent protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 78; 86pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY18307 standard; peptide; 44
                                                                                                                                  98WO-US022152.
                                                                                                                                                                      97US-00955636
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                                                                                                                                                                                                         (MINU ) UNIV MINNESOTA
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                                                                                                                                                                                                                                                                                   WPI; 1999-288309/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
                                                                                                                                                                                                                                               Nelsestuen GL;
                                                        WO9920767-A1.
                                                                                                                                                                    23-OCT-1997;
                                                                                                                              20-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33-OCT-1997;
                                                                                            29-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9920767-A1
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Query Match

Matches

à g G1y"

29-APR-1999

Synthetic

therapy

AAY18307;

RESULT 14 AAY18307

. 0

Gaps

0'

Length 44;

Example 1; Page; 58pp; English

The present sequence is the protein sequence of a mutated Gla domain (N-terminal amino acids 1-45) of human protein C. The mutated Gla domain contains the substitution mutations H100, S116 and S12N. Protein C and activated protein C variants comparising a mutated Gla domain are provided by the invention. The variants contain at least 6, and optionally 7-10, amino acid substitutions. A preferred mutant (designated GQNSEDY, see ABB19946) has the mutations H100, S116, S12N, D23S, Q32E, N33D and H44Y, and shows greatly enhanced anticoagulant activity in standard in vitro coagulation assays. The present mutant (designated QGNSEDY, see nexample from the invention as a step toward the production of the QGNSEDY mutant Gla domain, and shows little, if any, improvement in provides methods for producing the variants based on DNA technology, and with the use of the variants for the treatment of coagulation disorders such as thrombosis or APC resistance, or in diagnostic test systems for assaying components of the protein C-anticoagulant system (all claimed). The variants may also be used in treating arteriosclerosis, myocardial infarction, and disseminated intravascular coagulation. Note: The present sequence is not shown in the specification but is derived from the human wild-type Gla domain sequence given on page 7 of the specification (see ABB79947)

Sequence 45 AA;

Gaps .. Query Match 85.3%; Score 168; DB 5; Length 45; Best Local Similarity 72.7%; Pred. No. 1.6e-20; Matches 32; Conservative 3; Mismatches 9; Indels

1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIPEDVDDTLAFWSKH 44

ઠ

1 ANSFLEELROGNLERECIEEICDFEEAKEIFONVDDTLAFWSKH 44 g

Search completed: March 1, 2004, 10:01:23 Job time : 50 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

March 1, 2004, 09:59:33 ; Search time 13.5 Seconds
 (without alignments)
 313.513 Million cell updates/sec

SEQ1-4SUBS 197 1 ANSFLXXLRQGSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH

Title: Perfect score: Sequence:

44

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

TA TA	Description	protein C (activat	Ü	ບ	Ü	ijor	coagulation factor	coagulation factor	44		O	O		coagulation factor	Φ	plasma protein S p	٠		coagulation factor		tion	protein S	protein S	plasma protein S p	tion fact	.n (EC 3.4	plasma protein S p	protein Z	protein	arrest-spe
SUMMAKLES	E :	KXHU	JX0210	S18994	KXBO	EXRT	EXBO	EXHU	I46932	KFHU7	810511	A35827	EXCH	KFB07	S53434	KXHUS	TBHU	S38819	A30351	JQ0419	KFHU	KXBOS	S53433	KXRTS	KFBO	TBBO	KXMSS	KXB02	KXHUZ	A48089
	DB (¦	Н	٦	~	ч	ч	н	N	Н	N	~	-	-	(7		н	~	1	~	Н	H	0	ч	-	Н	н	-		0
	Length	461	461	461	456	482	492	488	443	466	617	618	475	407	642	676	622	646	452	459	461	675	642	675	416	625	675	396	422	673
d	% Query Match	81.2	71.1	70.6	61.9	58.4	57.9	٠	ä	50.3	m m	m,	43.7	43.1	43.1	43.1	•			•		•		39.6				35.3		33.0
	Score	160	4	'n	122	Н	н	$\overline{}$	0	თ თ	86.5	Ġ.	98	85	82	85	84	81	80	80	80	80	78	78	73	72	71		65.5	
	Result No.	-	7	m	4	'n	φ	7	00	σı	10	11	12	13	14	15	16	17	18	19	70	21	22	23	24	25	26	27	28	53

155476 155476 1548089 154859 154859 1740556 1740556 1725948 1739306	growth potentiatin	growen arrest-spec probable MAP kinas	probable MAP kinas	probable MAP kinas	hypothetical prote	hypothetical prote	protein-tyrosine k	hypothetical prote	ammonium transport	mitogen-activated	VSG expression sit	protein-tyrosine k	platelet-derived g	tyrosine kinase re	type II site-speci
	155476	4859	C96575	6763	T40556	T02367	8375	5948	2918	9306	2433	8999	3727	1189	NDECRS
	010	7 7	71	N	N	C)	~	N	7	N	N	~	Н	N	Н
	674	5 7 B	603	576	909	1684	1363	323	510	422	1235	1298	1089	182	245
6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	32.5	28.7	27.7	27.2	26.9	25.4	24.9	24.6	24.6	24.4	24.4	24.4	24.1	23.9	23.9
332.5 222.0 222.0 222.0 227.7 277.7 277.7 277.2	4,0	56.5	54.5	53.5	53	20	49	48.5	48.5	48	48	48	47.5	47	47
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	30	3 F	33	34	35	36	37	38	39	4.0	41	42	43	44	45

ALIGNMENTS

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A;Molecule type: mRNA
A;Residues: 1-461 <OKA2>
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                                                                                                    Query Match
Best Local S:
Matches 26,
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                                                                                                                                                              A;Geneelics:
A;Geneelics:
A;Geneelics:
A;Geneelics:
A;Cross-references: GDB:120317; OMIM:176860
A;Cross-references: GDB:120317; OMIM:176860
A;Cross-references: 42/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A;Map position: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
A;Introns: 24/1; 79/3; 88/1; 134/1; 179/1; 226/3; 266/1
C;Superfamily: coagulation factor X; EGF homology, Gla domain homology
C;Ceywords: anticoagulation; Deta-hydroxysapartic acid; blood coagulation; calcium binding
C;Superfamil: signal sequence #status predicted <SIG>C;Ceywords: anticoagulation; Deta-hydroxysapartic acid; blood coagulation; calcium binding
F;13-42/Domain: Gla domain homology <GIA>
F;33-42/Domain: Dropepide #status predicted <LCH>
F;20-413/Domain: EGF homology <EGS>
F;20-445/Domain: EGF homology <EGS>
F;20-445/Domain: activation peptide #status experimental <APT>
F;20-445/Domain: trypsin homology <EGS>
F;20-445/Domain: trypsin homology <EGS
F;20-445/Domain:
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A,Residues: 1-461 cALD.
A,Festdues: 1-61 cALD.
A,Experimental source: liver
C,Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.139-134/Domain: Der homology cEG2>
F.199-461/Domain: BGF homology cEG2>
F.199-461/Domain: activation peptide #status predicted <ACT>
F.199-41/Domain: activation peptide #status predicted <ACT>
F.199-21/Domain: activation peptide #status predicted <ACT>
F.212-461/Product: vitamin K-dependent serine proteinase #status predicted <VIT>
F.212-445/Domain: trypsin homology <TRX>
F.47,48.55.57.60.51.66.67.70,76/Modified site: gamma-carboxyglutamic acid (Glu) #status F.112/Modified site: erythro-beta-hydroxyapartic acid (App) #status predicted F.121-130,139-150,146-159,161-174,182-319,238-254,373-388-426/Disulfide bonds: #stat F.214,290,355/Binding site: carbohydrate (Asn) (covalent) #status predicted #status predicted
C;Comment: Protein C is synthesized in the liver as a single chain precursor, which is c
bin, which cleaves a dodecapeptide from the amino end of the heavy chain; this reaction,
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam; F; 1-33/Domain: signal sequence #status predicted <SIG> F; 27-85/Domain: dla domain homology <CILA> F; 34-41/Domain: propeptide #status predicted <PRO> F; 34-41/Domain: propeptide #status predicted <PRO> F; 42-196/Domain: light chain #status predicted <PRO> F; 42-196/Domain: BGF homology <BGI> F; 51-136/Domain: BGF homology <BGIP Homology <BGIP <
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N;Alternate names: vitamin K-dependent serihe proteinase
C;Species: Mus musculus (house mouse)
C;Species: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: ĴX0210
R;Tada, N.; Sato, M.; Tsujimuxa, A.; Iwase, R.; Hashimoto-Gotoh,
J. Biochem. 111, 491-495, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.2%; Score 160; DB 1; Length 461;
70.5%; Pred. No. 8.6e-18;
.ive 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 ANSFLEELRHSSLERECIEEICDFEEAKEIFQNVDDTLAFWSKH 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
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les 31; Conservative
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A;Cross-references: ENRL:X64336; NID:956962; PIDN:CAA45617.1; PID:956963
C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology
C;Keywords: beta-hydroxysapartic acid; glycoprotein; hydrolase; serine proteinase
C;Keywords: beta-hydroxysapartic acid; glycoprotein; hydrolase; serine proteinase
C;Keywords: beta-hydroxysapartic acid; glycoprotein; hydrolase; serine proteinase
F;1-32/Domain: dla domain homology <GLA>
F;3-44/Domain: EGF homology <GLA>
F;3-445/Domain: EGF homology <EG2>
F;1-39-174/Domain: EGF homology <EG2>
F;139-174/Domain: EGF homology <EG2>
F;131-174/Domain: EGF homology <EG2>
F;131-175/Domain: EGF homology <EG2>
F;131-175/
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C;Accession: Si8994, 824312
R;Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Submitted to the EMBL Data Library, February 1992
A;Description: The CDNA cloninig and mRNA expression of rat protein C.
A;Reference number: S18994
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NiAlternate names: autoprothrombin IIA; plasma protein C
CiSpecies: Bos primigenius tarus (cattle)
CiSpecies: Bos primigenius tarus (cattle)
CiDate: 30-Nov-1980 #sequence 16-Jul-1999
CiDate: 30-Nov-1980 #sequence 16-Jul-1999
Forc. Natl. Acad. Sci. US.A. 81, 563-5656, 1984
A;Thitle: Cloning and sequence of liver cDNA coding for bovine protein C.
A;Reference number: A26250; MUID:85014826; PMID:6091100
                                                                                                                                 Gaps
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A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-42 OKAA
A, Cross-references: EMBL:X64336; NID:g56962; PIDN:CAA45617.1; PID:g56963
R; Okafuji, T.; Maekawa, K.; Nawa, K.; Marumoto, Y.
Biochim. Biophys. Acta 1131, 329-332, 1992
A; Title: The CDNA cloning and mRNA expression of rat protein C.
A; Reference number: S24312; MUID:92329550; PMID:1627650
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            Length 461;
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                                                                                                                                                                                                                                                                                                               42 ANSFLEEMRPGSLERECMESICDFEEAQEIFQNVEDTLAFWIKY 85
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ch 71.1%; Score 140; DB 1; Similarity 59.1%; Pred. No. 1.5e-14; 26; Conservative 7; Mismatches 11.
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A; Residues: 1-456 < LON>
R; Fernlund, P.; Stenflo,
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Fig.20%/Product: coagulation factor X light chain #status predicted <LCH>
Fig.1179/Product: coagulation factor X light chain #status predicted <LCH>
Fig.121/Domain: BGF homology <EG1>
Fig.121/Domain: BGF homology <EG2>
Fig.32-164/Domain: BGF homology <EG2>
Fig.32-482/Product: coagulation factor X heavy chain #status predicted <HCH>
Fig.32-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>
Fig.32-485/Product: coagulation factor Xa heavy chain #status predicted <ACT>
Fig.32-485/Domain: trypsin homology <TRY>
Fig.32-460/Domain: trypsin homology <TRY>
Fig.32-490/Bastatic acibohydrate (Asn) (covalent) #status experimental Fig.38-402,41:
Fig.31/Cleavage site: carbohydrate (Asn) (covalent) #status predicted Fig.32/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #status Fig.31/Cleavage site: His, Asp, Ser #status predicted
                                                                                                                                                                                                       A)Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
A;Note: submitted to the EMBL Data Library, June 1994
A;Note: nather the complete nucleic acid sequence nor the complete translation are shown R;Stanton, C.; Ross, R.P.; Hutson, S.; Wallin, R.
Gene 169, 269-273, 1996
A;Title: Processing and expression of rat and human clotting factor-X-encoding cDNAs.
A;Reference number: UC4670; MUID:96194815; PMID:8647460
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BEDLYO'L, K.; Miyazaki, K.; Kato, H.
J. Biochem. 109, 890-898, 1991
A.Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat plan
A.Reference number: PS0190; MUID:92041742; PMID:1718949
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A; Description: catalyzes the proteolytic activation of prothrombin to thrombin in the preparation of catalyzes the proteolytic activation of prothrombin to thrombin in the preparation; blood coagulation factor X; EGF homology; Gla domain homology; trypsin homology C; Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam: F; 1-31/Domain: signal sequence #status predicted <SIG> F; 4-40/Domain: propeptide #status predicted <PRO> F; 4-40/Domain: propeptide #status predicted <PRO> F; 4-10/Domain: Gla domain homology <GLA> F; 4-10/Domain: GPF homology <GLA> F; 4-1
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A; Mesidues: 183-186, X', 188-207 < ENU2>
B; Murakawa, M.; Okamura, T.; Kamura, T.; Kuroiwa, M.; Harada, M.; Niho, Y.

Eur. J. Haematol. 52, 162-168, 1994
A; Title: Analysis of the partial nucleotide sequences and deduced primary structures of A; Reference number: 146196; MUID:94222160; PMID:8168596
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N,Alternate names: Stuart factor
C,Species: Bos primigenius taurus (cattle)
C,Date: 24-Apr-1984 #sequence_revision 17-Mar-1987 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-482 <STA2>
A;Cross-references: EMBL:X79807; NID:9506600; PIDN:CAA56202.1; PID:9506601
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A;Molecule type: DNA
A;Residues: 295-383, 'G', 385-455 <MUR>
A;Cross-references: GB:D21215; NID:g415309; PIDN:BAA04756.1; PID:g455396
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A; Residues: 41-58, 'X', 60-65 < ENJ1>
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Best Local Similarity 43.2'
Matches 19, Conservative
                                                                                                                                                               1-482 <STA1>
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C;Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin C;Superfamily: cagailation factor X; EGF homology; Gla domain homology; trypsin homology (Keywords: anticoagulant; beta-hydroxyaspartic acid; blood coagulation; calcium binding F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>F;24-35/Domain: Gla domain homology <GGLA>F;30-39/Domain: Gradmain homology <GGLA>F;30-39/Domain: propeptide #status predicted <PRO>F;30-39/Domain: BGF homology <GGLA>F;31-144/Domain: BGF homology <GGLA>F;31-144/Domain: EGF homology <EGGL>F;31-144/Domain: trypsin homology <EGGL>F;31-144/Domain: trypsin homology <EGS-F;31-144/Domain: trypsin homology <EGS-F;31-148/Ja4-157,159-172,180-318,237-253,368-382,393-421/Disulfide bonds: #status F;119-122,137-148,144-157,159-172,180-318,237-253,368-382,397/Active site: His, Asp, Ser #status predicted
F;366/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Recession: A18386; MUID:83007326; PMID:6896877
A;Recession: A18386; MUID:83007326; PMID:6896877
A;Recession: A18386; MUID:83007326; PMID:6896877
A;Residues: 197-454; PVV (STE>
R;Resmon, N.L.; DeBault, L.E.; Esmon, C.T.
B; Bsmon, N.L.; DeBault, L.E.; Esmon, C.T.
A;Reference number: A3754; MUID:83213513; PMID:6304092
A;Title: Proteolytic formation and properties of gamma-carboxyglutamic acid-domainless particle: Proteolytic formation, and properties of gamma-carboxyglutamic acid-domainless particle: Esmon, N.L.; Laue, T.M.; Esmon, C.T.
J; Biol. Chem. 258, 5554-5560, 1983
A;Title: Structural changes required for activation of protein C are induced by Ca2+ bir A;Reference number: A37542; MUID:83213514; PMID:6405603
A;Reference number: A37542; MUID:83213514; PMID:6405603
C;Comment: Protein C is the zymogen of the vitamin K-dependent serine proteinase that re
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C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000
C;Date: 31-Jan-1995 #sequence revision 07-Feb-1997 #text_change 08-Dec-2000
C;Datession: S49075; JC4670; FS0191; PS0190; I62745
R;Stanton, C.; Ross, P.; Hutson, S.; Wallin, R.
Thromb. Res. 80, 63-73, 1995
A;Title: Evidence for competition between vitamin K-dependent clotting factors for intra
A;Reference number: A58498; MUID:96093366; PMID:8578539
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J. Biol. Chem. 257, 12170-12179, 1982

A,Title: Amino acid sequence of the light chain of bovine protein C. A,Reference number: A18385; WUID:83007325; PMID:6896876

A,Accession: A18385

A,Molecule type: protein
A,Residues: 40-194 «FER.
A,Note: 82-Lys was also found
R,Drakenberg, T.; Fernlund, P.; Reepstorff, P.; Stenflo, J.
A,Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C. A,Title: beta-Hydroxyaspartic acid in vitamin K-dependent protein C. A,Reference number: A19316; WUID:83169769; PMID:6572939
A,Contents: annotation; revision to residue 110
R,Stenflo, J.; Fernlund, P.
J. Biol. Chem. 257, 12180-12190, 1982
A,Title: Amino acid sequence of the heavy chain of bovine protein C. A, Reference number: A18386; WUID:831007326; PMID:6896877
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Pred. No. 1.2e-11;
9; Mismatches 12; Indels
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Residues: 1-487 <FUN> Accession: A22867

Accession: A14997

seq1-4subs.rpr

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'Species: Homo sapiens (man)
'Date: 15-Nov-1984 #sequence_revision 02-May-1994 #text_change 08-Dec-2000
'Accession: A4478; J09031; A42485; A2853; A22208; A21284; A20362; S39415; I54051; A00'; Acchemistry S.P.; Foster, D.C.; Krrachi, K.; Davie, E.W.
iochemistry 25, 5098-5102, 1986
'Title: Gene for human Factor X: a blood coagulation factor whose gene organization is Reference number: A24478; MUID:87026600; PMID:3768336
                                                              the proteolytic activation of prothrombin to thrombin in the pr
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A; Residues 1.488 cLEX-
A; A: Residues 1.488 cLEX-
A; Cross-references: GB: L29433; GB: M14327; NID: g459809; PIDN: AAA52764.1; PID: g182831
A; Cross-references: GB: L29433; GB: M14327; NID: g459809; PIDN: AAA52764.1; PID: g182831
B; Messier, T.L.; Pittman, D.D.; Long, G.L.; Kaufman, R.J.; Church, W.R.
A; Messier, T.L.; Pittman, D.D.; Long, G.L.; Calls of a full-length cDNA encoding human coag
A; Reference number: JQ0917; MUID: 91216473; PMID: 1902434
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A/Residues: 1-488 <MES>
A/Cross-references: GB MS7285; NID:g182389; PIDN:AAA52421.1; PID:g182390
A/Cross-references: GB NF, Chung, D.W.; Davie, E.W.
X:Miao, C.H.; Leytus, S.P.; Chung, D.W.; Davie, E.W.
T. Biol. Chem. 267, 7395-7401, 1992
A/Title: Liver-specific expression of the gene coding for human factor X, a blood coagul
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A; Title: Isolation and characterization of human blood-coagulation factor X cDNA.
A; Reference number: A25853; MUID:86221713; PMID:3011603
A; Accession: A25853
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A;Note: sequence extracted from NCBI backbone (NCBIN:93780, NCBIP:93787)
R;Kaul, R.K.; Hildebrand, B.; Roberts, S.; Jagadeeswaran, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.9%; Score 114; DB 1; 45.5%; Pred. No. 2.4e-10;
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A;Residues: 19-284,'E',289-488 <KAU>
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Best Local Similarity 45.5%
20; Conservative
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A/Wolecule type: protein
A/Rolecule type: protein
A/Rolecule bype: protein
A/Rolecule carbohydrate binding sites
B/Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; L
Biochemistry 11, 4899-4903, 1972
A/Titani, K.; Hermodson, M.A.; Fujikawa, K.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.; L
Biochemistry 11, 4899-4903, 1972
A/Titale: Bovine factor K. B.W.
Proc. Natl. Acad. Sci. U.S.A. 72, 3359-3363, 1975
A/Ritle: Activation of bovine factor X (Stuart factor): conversion of factor Xaalpha to
A/Rolecence number: A15504; MUD: 76053121; PMID: 1059122
A/Contents: annotation; activation
B/Sugo, T.; Bjork, I.; Holmgren, A.; Stenflo, J.
J. Biol. Chem. 259, 5705-5710, 1984
A/Title: Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic
A/Contents: annotation; calcium binding
A/Rolecence number: A38024; MUD: 84185716; PMID: 5546930
A/Contents: annotation; calcium binding
C/Contents: annotation; sulfate binding
C/Comment: Factor Xa converts prothrombin to thrombin during blood clotting.
C/Comment: The two chains are formed from a single-chain precursor by the excision of tw
A/Title: The activation peptide is cleaved by factor IXa (in the intrinsic pathway), c
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lInoue, K.; Morita, T.
lachem. 218, 153-163, 1993
litie: Identification of 0-linked oligosaccharide chains in the activation peptides of
Reference number: S39414, MUID:94062825; PMID:8243461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: protein
Residues: 183-292,294-295,'GDE',299-334,336-348,'AE',351-354,356-441,'GKFG',446-492 <1
Note: carbohydrate binding sites and disulfide bonds were determined
Persson, E.; Selander, M.; Linse, S.; Drakenberg, T.; Oehlin, A.K.; Stenflo, J.
Biol. Chem. 264, 16897-16904, 1989
Title: Calcium binding to the isolated beta-hydroxyaspartic acid-containing epidermal
Reference number: A34412; MUID:89380326; PMID:2789221
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;;Comment: Calcium binds to the gamma-carboxyglutamic acid (Gla) residues and, with strd
};Comment: The gamma-carboxyglutamic acid residues arise by a posttranslational, vitamin
'Accession: A22867; A14997; A12030; A34412; S39414; A00925
; Pung, M.R.; Campbell, R.M.; MacGillivray, T.A.
ucoleic Acids Res. 12, 4481-4492, 1984
; Title: Blood coaqulation factor X mRNA encodes a single polypeptide chain containing
; Reference number: A22867; MUID:84247315; PMID:6330671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Morecule type: protein
"Readdues: 41-102,'N',104-180 cENF>
"Readdues: 41-102,'N',104-180 cENF>
"McMullen, B.A.; Fujikawa, K.; Kisiel, W.
"John Blophys. Res. Commun. 115, 8-14, 1983
"Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood cylcontents: annotation; revision to residue 103
"Fitean, K.; Fujikawa, K.; Enfield, D.L.; Ericsson, L.H.; Walsh, K.A.; Neurath, H.
"Foo. Natl. Acad 20: U.S.A. 72, 3082-3086, 1975
"Title: Bovine factor X-1 (Stuart factor): amino-acid sequence of heavy chain.
"Reference number: Al2030; MUID:76053069; PMID:1059093
                                                                                                                                                                                                                                                                                    Cross-references: GB:X00673; NID:g192; PIDN:CAA25286.1; PID:g193
Enfield, D.L.; Bricsson, L.H.; Fujikawa, K.; Walsh, K.A.; Neurath, H.; Titani, K.
cochemistry 19, 659-667, 1980
iffile: Amino acid sequence of the light chain of bovine factor X-1 (Stuart factor).
Reference number: A14997; MUID:80130563; PMID:6766735
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Molecule type: protein Residues: 85-126 <PER>

Accession: S39414

ccession: A34412

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Cagulation factor VIIa (EC 3.4.21.21) precursor [validated] - human C.Species: Homo sapiens (man) Saconaction (man) Saconactio
                                        F;103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental F;199,211/Binding site: carbohydrate (Thr) (covalent) #status experimental F;221,231/Binding site: carbohydrate (Asn) (covalent) #status experimental F;234-235/Cleavage site: Arg-Ile (coagulation factor IXa, coagulation factor VIIa) #stat F;276,322,419/Active site: His, Asp, Ser #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chrochers, A.B.; Clarke, B.J.; Sheffield, W.P.; Blajchman, M.A.
Thromb. Res. 69, 231-238, 1993
Abrittle: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A.Fittle: Complete nucleotide sequence of the cDNA encoding rabbit coagulation factor VII
A.Feference number: 146932, MUID:93190306; PMID:8383365
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: 1-443 < REO>
A.Status: The Coagulation factor X; EGF homology; Gla domain homology; trypsin homology; G.Staperfamily: coagulation factor X; EGF homology; Gla domain homology cBGL>
F.24-83/Domain: EGF homology cBGL>
F.130-166/Domain: EGF homology cBGL>
F.192-425/Domain: trypsin homology cTRY>
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*A/Reference number: A90539; MUID:89088153; PMID:3264725
A/Accession: A31186
A/Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Species: Oryctolagus cuniculus (domestic rabbit)
|Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Feb-1999
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1.1e-09;
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                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.8%; Score 110; DB Best Local Similarity 43.2%; Pred. No. 1.1e-Matches 19; Conservative 9; Mismatches
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mes 19; Conservative
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Residues: 11-284, E', 289-488 <LE2>
(Cross-references: GB: K01886
McMullen, B.A.; Fujikawa, K.; Kisiel, W.; Sasagawa, T.; Howald, W.N.; Kwa, E.Y.; Weins iochemistry 22, 2875-2884, 1983
iltle: Complete amino acid sequence of the light chain of human blood coagulation fact Reference number: A20362; MUID:83257207; PMID:6871167
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1r. J. Biochem. 218, 153-163, 1993
Title: Identification of O-linked oligosaccharide chains in the activation peptides of
Reference number: S39414; MUID:94062825; PMID:8243461
                                                                                                                                                                                             for human blood coagulati
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R)Padmanabhan, K.; Padmanabhan, K.P.; Tulinsky, A.; Park, C.H.; Bode, W.; Huber, R.; Blad. Mol. Biol. 222, 947-966, 1993
A)Title: Structure of human dest[145] factor Xa at 2.2 angstroms resolution.
A)Reference number: A49456; MUID:93360277; PMID:835279
A)Contents: annotation; X-ray crystallography, 2.2 angstroms
C)Comment: The two chains held together by one disulfide bond are formed from a single-c
C)Comment: The activation peptide is cleaved by factor IXa (in the intrinsic pathway) on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: glycosylation sites
A; Note: identification sites
A; Note: identification and characterization of beta-hydroxyaspartic acid
A; Note: identification and characterization of beta-hydroxyaspartic acid
B; Jagadeeswaran, P.; Reddy, S.V.; Rao, K.J.; Hamsabhushanam, K.; Lyman, G.
Gene 84, 517-519, 1989
A; Title: Cloning and characterization of the 5' end (exon 1) of the gene encoding human
A; Reference number: 154051; MUID: 90128299; PMID: 2612918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pd
A;Cross-references: GB:M22613; NID:9180335; PIDN:AAA51984.1; PID:9180336 Proc. Natl. Acad. Sci. US.A. 82, 3591-3595, 1985.
Proc. Natl. Acad. Sci. US.A. 82, 3591-3595, 1985.
A;Title: Characterization of animost full-length cDNA coding for human A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Reference number: A22208; MUID:85216545; PMID:2582420
A;Residues: 13-441, S',443-488 <FUN>
A;Residues: 15-441, S',443-488 <FUN>
A;Cross-references: GB:K03194; NID:9182840; PIDN:AAA52490.1; PID:9182841
B;Leytus, S.P.; Chung, D.W.; Kisell, W; Kuracchi, K.; Davie, B.W.
A;Title: Characterization of a cDNA coding for human factor X.
A;Reference number: A21284; MUID:84222026; PMID:6587384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: 154051
A;Status: translation not shown; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-23 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Map position: 13q34-13q34
introns: 24/1; 77/3; 86/1; 124/1; 150/3; 249/3; 289/1;
Note: deficiency of this factor causes Stuart disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Gene: GDB:F10
;Cross-references: GDB:119890; OMIM:227600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: protein
Residues: 183~234 <INO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecule type: protein
Residues: 41-179 <MCM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: S39415
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Gaps

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thrombin (EC 3.4.21.5) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: A58827; A42686; S12081
R;Degen, S.J.F.; Schaefer, L.A.; Jamison, C.S.; Grant, S.G.; Fitzgibbon, J.J.; Pai, J.A.
A)MA Cell Biol. 9, 487-498, 1990
A)MA Cell Biol. 9, 487-498, 1990
A)Title: Characterization of the cDNA coding for mouse prothrombin and localization of the A;Reference number: A35827; MUID:91025551; PMID:2222810
                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rosedeuse: 383-617, E' < CADA>
A;Cosedeuse: 383-617, E' < CADA>
A;Cosedeuse: 383-617, E' < CADA>
A;Crosedeuse: 08:M81397
C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C;Superfamily: thrombin; Galcium binding; carboxyglutamic acid; glycoprotein; hydr
F;1-24/Domain: signal sequence #status predicted < CADA>
F;25-43/Domain: propeptide #status predicted < CADA>
F;28-88/Domain: propeptide #status predicted < CADA>
F;28-88/Domain: Cada domain homology < CADA>
F;28-88/Domain: Cada domain homology < CADA>
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A)Status: preliminary
A)Anolecule type: mRNA
A)Anolecule type: mRNA
A)Ascascinates: 1-618 < DEGS>
A)Cross-references: GB:X52308; NID:g53813; PIDN:CAA36548.1; PID:g53814
A)Cross-references: GB:X52308; NID:g53813, 6
A)Cross-references: GB:X52308; NID:S7816
A)Note: the data were obtained from females resulting from the cross of M. domesticus an R;Banfield, D.K.; MacGillivray, R.T.A.
B;Banfield, D.K.; MacGillivray, R.T.A.
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq
A;Reference number: A42696; MUID:92212913; PMID:1557383
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A Molecule type: mRNA
A Cross-references: GB:881394
C Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology
C Keywords: blood coaquiation; calcium binding; carboxyglutamic acid; glycoprotein; hydr
C F:124/Domain: propeptide #status predicted < SIG>
F:22-43/Domain: propeptide #status predicted < PRO>
F:28-88/Domain: Gla domain homology < GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;44-617/Froduct: prothrombin #status experimental <PMAT>
F;40-187/Domain: kringle homology <RR1>
F;109-187/Domain: kringle homology <RR2>
F;109-187/Domain: kringle homology <RR2>
F;100-609/Domain: trypsin homology <TRY>
F;100-18,58.60,63,64.69,70,73,76,76/Modified site: gamma-carboxyglutamic acid (Glu) #status
F;61-66,91-104,109-187,130-170,158-182,215-292,236-276,264-287,332-478,387-403,532-546,5
F;402,458,564/Active site: His, Asp, Ser #status predicted
                   A;Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat ute R;Banfield, D.K.; MacGillivray, R.T.A. A;Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992
A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq A;Reference number: A42696; MUID:92212913; PMID:1557383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%; Score 86.5; DB 2; Length 617; 42.2%; Pred. No. 8.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19; Indels
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A, Residues: 44-58 < HEN>
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A; Residues: 213.466 TH2>
A; Residues: 213.466 TH2>
B; Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
J. Bjoern, S.; Foster, D.C.; Thim, L.; Wiberg, F.C.; Christensen, M.; Komiyama, Y.; Peder
A; Title: Human plasma and recombinant factor VII. Characterization of O-glycosylations a
A; Reference number: Adology, MUD: 91250411; PMID: 1904059
A; Reference number: Amountation; carbohydrate binding sites
B; Persson, E.; Petersen, L.C.
Biochem. 234, 293.300, 1995
A; Ritle: Structurally and functionally distinct Ca(2+) binding sites in the gamma-carbox
A; Reference number: S63524; MUD: 96096752; PMID: 8529655
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R;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.
Endocrinology 126, 167-175, 1990
A;Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.
A;Reference number: A60576; MUID:90091942; PMID:2293980
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$10511

C. 50 details (EC 3.4.21.5) precursor - rat
C. 50 pectes: Rattus norvegicus (Norway rat)
C. 50 ate: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C. 50 ate: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C. 50 ate: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C. 50 ate: 07-May-1993 #sequence revision 07-May-1993 #text_change 03-May-2002
C. 50 ate: 07-May-1993 #sequence 05 Fat prothrombin.
A. 50 ate: 07-May-1993 #text_change 03-May-2002
A. 50 ate: 07-May-2002
A. 50 ate: 
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48.8%; Pred. No. 6.1e-08;
tive 4; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 61-65;99-103;105-109;213-217;308-312 <PER>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Conservative
A; Residues: 61-212 <THI>
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Residues: 1-617 <DIH>
                                           Accession: B31186
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Best Local
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Gaps

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F;44-618/Product: prothrombin B #status predicted <MAT>
F;109-187/Domain: kringle homology <KR1>
F;109-187/Domain: kringle homology <KR2>
F;215-293/Domain: trypsin homology <TRY>
F;561-610/Domain: trypsin homology <TRY>
F;561-66,91-104,109-187,130-170,158-182,215-293,236-276,264-288,333-479,388-404,533-547,5
F;403,459,565/Active site: His, Asp, Ser #status predicted
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A Note: structure and location of covalently bound carbohydrate

G;Function:

A;Description: catalyzes the protecolytic activation of coagulation factor X in the present gulation factor IX in the presence of calcium and tissue factor

A;Pathway: blood coagulation extrinsic pathway

G;Superfamily: coagulation factor X; EGF homology, Gla domain homology; trypsin homology

G;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F;1-152/Product: coagulation factor VIIa light chain #status experimental <MA1>

F;50-61/Domain: GIA domain homology (fragment) <GIA>

F;91-127/Domain: EGF homology <EG2>
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Fil53-407/Product: coagulation factor VIIa heavy chain #status experimental <MA2>
Fil53-387/Domain: trypsin homology <TRY>
Fil53-387/Domain: trypsin homology <TRY>
Fil53-146,19.20,25,56.29,34.316.329,340.316 site: gamma-carboxyglutamic acid (Glu) #status Fil7-22,50-61,55-70,72-81,91-102,98-112,114-127,135-262,159-164,178-194,310-329,340-368/1 Fi52/Binding site: carbohydrate (Ser) (covalent) #status experimental Fi145,203/Binding site: carbohydrate (Asn) (covalent) #status experimental Fi152-153/Cleavage site: Arg-Ile (coagulation factor XIIa) #status experimental Fi152-153/Cleavage site: His, Asp. Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Molecule type: protein
A; Residues: 58-62, XX, 64-68 < MCM>
A; Residues: 58-62, XX, 64-68 < MCM>
A; Note: the residue designated 'X' was determined to be hydroxyaspartic acid
B; Hase, S; Kawabata, S; Nishimura, H; Takeya, H; Sueyoshi, T.; Miyata, T.; Iwanaga, J. Blochem. 104, 867-868, 1988
A; Else, A new trisaccharide sugar chain linked to a serine residue in bovine blood coagn
A; Reference number: A4556; WUID:89213999; PMID:3149637
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasma protein S precursor, vitamin K dependent - rhesus macaque (fragment) (Species: Macaca mulatta (rhesus macaque) (Species: Macaca mulatta (rhesus macaque) (C)Species: Macaca mulatta (rhesus macaque) (C)Species: Macaca mulatta (rhesus macaque) (C)Accession: 853434 (B)Species: Macaca mulatta (R)Species (M)Species (
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F;1-7/bomain: signal sequence (fragment) #status predicted <SIG>
F;8-642/Product: plasma protein S #status predicted <MAT>
F;87-120//bomain: EGF homology <EG1>
F;127-165/Domain: EGF homology <EG2>
                                                                                                                                             A,Molecule type: protein
A,Residues: 1-407 <TAK>
Residues: 1-407 <TAK>
A;Residues: 1-407 <TAK>
A;Residues: 1-407 <TAK>
B,MoMuller, B.A., Fujikawa, K.; Kisiel, W.
Biochem. Blophys. Res. Commun. 115, 8-14, 1983
Biochem. Biophys. Res. Commun. 115, 8-14, 1983
A,Title: The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood co. A;Reference number: A20274; MUID:83308813; PMID:6688526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW 41
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                     A; Reference number: A31979; MUID: 89008362; PMID: 3049594
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A; Residues: 1-642 <GRES-
A; Cross-references: EMBL:131380
A; Experimental source: tissue type liver
A; Note: the source is designated as rhesus monkey
                                                                                    A; Accession: A31979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coagulation factor Xa (EC 3.4.21.6) precursor - chicken
NiAlternate names: virus-activating proteinase
C;Spaces: Gallue gallue (chicken)
C;Date: 12-Feb-1993 #sequence revision 07-Feb-1997 #text_change 16-Jul-1999
C;Accession: S15838; S20380; S20381
K;Suzuki, H.; Harada, A.; Hayashi, Y.; Wada, K.; Asaka, J.; Gotoh, B.; Ogasawara, T.; Na FEBS Lett. 283, 281-285, 1991
A;Title: Primary structure of the virus activating protease from chick embryo. Its ident A;Reference number: S15838; MUID:91257322; PMID:2044767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Molecule type: mRNA
A.Residues: 1-475 <SUZ>
A.Cross-references: DD31:D00844; NID:g222869; PIDN:BAA00724.1; PID:g222870
R.forob, B.; Yamauchi, F.; Ogasawara, T.; Nagai, Y.
FEBS Lett. 296, 274-278, 1992
A.Title: Isolation of factor Xa from chick embryo as the amniotic endoprotease responsib
A.Reference number: S20380; MUID:92164779; PMID:1537403
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(Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

(Skywcrde: coagulation factor X; EGF homology; Gla domain homology; trypsin homology

(Skywcrde: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam

F)1-20/Domain: signal sequence #status predicted <SIG>

F)21-40/Domain: propeptide #status predicted <PRO>

F)25-84/Domain: Gla domain homology <GIA>

F)41-185/Product: coagulation factor X light chain #status experimental <LCH>

F)90-121/Domain: EGF homology <EGI>
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J. Biol. Chem. 263, 14868-14877, 1988
A;Title: Bovine factor VII. Its purification and complete amino acid sequence.
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C.Species Bos prinigenius raurus (cattle)
C.Date: 21-May-1990 #sequence_revision 23-Mar-1995 #text_change 16-Jul-1999
C.Accession: A31979; C20274
                                                                                           Gaps
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                                                                                                                                                                                                     1 ANS-FLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                 44 ANSGPLEELRKGNLERECVEEQCSYEEAFFALESPQDTDVFWAKY 88
                                                                             19; Indels
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       42.2%; Pred. No. 8.4e-06;
tive 6; Mismatches 19
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A;Residues: 241-246,'X',248-251,'X',253-261 <GOT>
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Best Local Similarity 40.5'
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A;Residues: 41-55 <GO2>
A;Accession: S20381
Best Local Similarity
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Note: the authors translated the codon TTT for residue 26 as Leu
Floos van Amstel, H.K.; Reitsma, P.H.; van der Logt, C.P.E.; Bertina, R.M.
cohemistry 29, 7853-7861, 1990
Title: Intron-exon organization of the active human protein S gene PSalpha and its pse
Reference number: A35611; MUID:91084445; PMID:2148111
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Hoskins, J.; Norman, D.K.; Beckmann, R.J.; Long, G.L.
Coc. Natl. Acad. Sci. U.S.A. 84, 349-353, 1987
Jitle: Cloning and characterization of human liver cDNA encoding a protein S precursor Reference number: A26157; MUID:87092407; PMID:3467362
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A, Accession: A25891
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Cross-references: 27-220,'L', 222-262,'H', 264-344,'Y', 346-676 < LUN>
A, Cross-references: GB: M14338; NID: 9190448; PIDN: AA460181.1; PID: 9190449
A, Note: part of this sequence, including the amino end of the mature protein, was determ
B, Edenbrandt, C.M.; Lundwall, A; Wydro, R.; Stenflo, J.
Biochemistry 29, 7861-7668, 1990
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A;Title: Two genes homologous with human protein S cDNA are located on chromosome 3. A;Title: Two genes homologous with human protein S cDNA are located on chromosome 3. A;Reference number: A60903; MuID:88178564; PMID:2895503
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A;Reference number: A35610; MUID:91084444; PMID:2148110
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A;Residues: 351-676 <PLO>
R;Ploos van Amscl. H.K.; van der Zanden, A.L.; Reitsma, P.H.; Bertina, R.M.
FEBS Lett. 222, 186-190, 1987
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F;171-207/Domain: EGF homology <EG3>
F;213-248/Domain: EGF homology <EG4
F;281-633/Domain: sex hormone-binding globulin homology <SHB>
F;291-444/Domain: laminin G repeat homology <LGR>
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A,Residues: 284-676 <EDE>
A,Cross-references: GB:J02919
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Residues: 1-676 <SCH>
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A;Residues: 1-25 <PL3>
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Albescription: a cofactor for activated protein C (EC 3.4.21.69); thrombin cleavage dest C.f.Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom C.f.Seywords: beta-hydroxyasparagine; beta-hydroxyasparagine; beta-hydroxyasparagine; beta-hydroxyasparagine; beta-hydroxyasparagine; acta-hydroxyasparagine; acta-hydroxyasparagine; beta-hydroxyasparagine; beta-hydroxyasparagine; beta-hydroxyasparagine; sequence #status predicted <SIG>F:24.70Dmain: propeptide #status predicted <FRO>F:26.85/Domain: Gla domain homology <GLA>F:26.85/Domain: Gla domain homology <GLA>F:26.85/Domain: Gla domain protein S #status predicted <MAT>
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47,325-478(5.61.66.57.70.77.77) Modified site: gamma-carboxyglutamic acid (Glu) #stat F;47,48.55.57.60.61.66.57.70.77.77 Modified site: gamma-carboxyglutamic acid (Glu) #stat E;58-63.88-113.121-134,126-143.145-154.161-175.171-184.186-199,205-217,212-226,228-241,2 F;111-112/Cleavage site: Arg-Ser (thrombin) #status predicted F;136/Modified site: erythro-bera-hydroxyasparaqine (Asn) #status predicted F;499,509,530/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Cross-references: GDB.120721, OMIM:176880
A,Map position: 3pl1.1-3ql1.2
A,Introns: 26/1, 78/3, 87/1, 116/1, 157/1, 201/1, 243/1, 283/3; 322/2, 385/3, 441/3; 498
C;Complex: in plasma forms a complex with C4b binding protein
A, Title: Human protein S cDNA encodes Phe-16 and Tyr 222 in consensus sequences for the
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A;Residues: 1-676 <PL2>
A;Cross-references: EMBL:Y00692; NID:g36578; PIDN:CAA68687.1; PID:g36579
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43.1%; Score 85; DB 1; Length 676;
Best Local Similarity 38.6%; Pred. No. 1.6e-05;
Matches 17; Conservative 10; Mismatches 17; Indels
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F;121-154/Domain: EGF homology <EG1>
F;161-199/Domain: EGF homology <EG2>
F;205-241/Domain: EGF homology <EG3>
F;247-282/Domain: EGF homology <EG3>
F;347-282/Domain: EGF homology <EG4>
F;315-667/Domain: sex hormone-binding globulin homology <SHB>
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                                         Reference number: S02424; MUID:88005138; PMID:2820795
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GenCore version 5.1.6
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OM protein - protein search, using sw model

SEQ1-4SUBS 197 1 ANSPLXXLRQGSLXRXCIXX.....XXAKXIFedVDDTLAFWSKH 44

Title: Perfect score: Sequence:

Scoring table:

141681 seqs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		mus n				bos t	P00743 bos taurus	P00742 homo sapien	Q9bzd7 homo sapien	O19045 oryctolagus	P98139 oryctolagus	homo	O14668 homo sapien	rattu	mus mu		bos ta	Q28520 macaca mula	P07225 homo sapien	Q9bzd6 homo sapien	P83370 hoplocephal	P00734 homo sapien	P81428 tropidechis	oryg	gnw	cani	น ธกม	homo	pan t	pog	rat		not
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ALIGNMENTS

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Reitsma P.H., Poort S.R., Allaart C.F., Briet E., Bertina R.M.; "The spectrum of genetic defects in a panel of 40 Dutch families with symptomatic protein C deficiency type I: heterogeneity and founder
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MEDIATRE-29205321, PubMed=1611081;
Sugahara Y., Miura O., Yuen P., Aoki N.;
"Protein C deficiency Hong Kong I and 2: hereditary protein C deficiency caused by two mutant alleles, a 5-nucleotide deletion and a missense mutation";
Blood 80:126-131(1992).
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WEDLINE-92380661; PubMed=1511989;
MEDLINE-92380661; PubMed=1511989;
"Tuby C.B., Schulman S., Tengborn L., Kakkar V.V., Cooper D.N.;
"Two different missense mutations at Arg 178 of the protein C (PROC)
gene causing recurrent venous thrombosis.";
Hum. Genet. 89:685-686(1992).
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Yamamoto K., Matsushita T., Sugiura I., Takamatsu J., Iwasaki E.,
Mada H., Deguchi K., Shirakawa S., Saito H.;
Homozygous protein C deficiency: identification of a novel missense
mutation that causes impaired secretion of the mutant protein C.";
J. Lab. Clin. Med. 119:682-689(1992).
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MEDLINE=92371391; PubMed=8499565;
Poort S.R., Pabinger-Fasching I., Mannhalter C., Reitsma P.H.,
Bertina R.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92380660; PubMed=1511988; grandy C.B., Chisholm M.; Karkar V.V., Cooper D.N.; A novel homozygous miseense mutation in the protein C (PROC) gene causing recurrent venous thrombosis.";
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WEDLINE-923260852.

Gandrille S., Vidaud M., Aiach M., Alhenc-Gelas M., Fischer A.M.,
Gouault-Heilman M., Toulon P., Fiessinger J.N., Goossens M.;
TWO novel mutations responsible for hereditary type I protein C
deficiency: characterization by denaturing gradient gel
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Blood Coagul. Fibrinolysis 4:273-280(1993).
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Blood 79:1456-1465(1992).
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MEDLINE-92190481; PubMed=1347706;
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MEDLINE=93271396; PubMed=8499568;
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                            Sanchez A.,
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"The 2.8 A crystal structure of Gla-domainless activated protein C.";
EMBO J. 15:6822-6831(1996).
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Thromb. Haemost. 69:77-84(1993).
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Mather T., Oganessyan V., Hof P., Huber R., Foundling S., Bsmon C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90293094; PubMed=1694199;
Miletich J.P., Broze G.J. Jr.;
Beta protein C is not glycosylated at asparagine 329. The rate of
translation may influence the frequency of usage at asparagine-X-
cysteine sites.";
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Proc. Natl. Acad. Sci. U.S.A. 84:2829-2832(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C London 1: recurrent mutation at Arg-169 (CGG-->TGG) in
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Reitsma P.H., Poort S.R., Bernardi F., Gandrille S., Long G.L.,
Sala N., Cooper D.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87204221; PubMed-2437584;
Romeo G., Hassan H.J., Staempfli S., Roncuzzi L., Cianetti L.,
Leonardi A., Vicente V., Mannucci P.M., Bertina R.M., Peschle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90098906; PubMed=2602169;
Grundy C.B., Chitolie A., Talbot S., Bevan D., Kakkar V.V.,
Cooper D.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 106-461 FROM N.A.
MEDLINE-84772714; PubMed=6589623;
Foster D.C., Davie E.W.;
"Characterization of a cDNA coding for human protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:4766-4770(1984).
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Nucleic Acids Res. 17:10513-10513(1989).
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MEDLINE=91329836; PubMed=1868249;
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                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/SvJ;
MEDLINE=98152576; PubMed=9493582;
Malbert L.R., Rosen B.D., Lissens A., Carmeliet P., Collen D.,
Castellino F.J.;
"Nucleotide structure and characterization of the murine gene encoding anticoagulant protein C.";
Thromb. Haemost. 79:310-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBDIVITY: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.

FIRSUE SPECIFICITY: Plasma; synthesized in the liver.

FTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.

MISCELLANBOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   region of mammalian protein C.";
Br. J. Haematol. 86:590-600(1994).
-!- CHUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa.
                                    Gaps
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Murakawa M., Okamura T., Kamura T., Kurciwa M., Harada M., Niho Y.;
"A comparative study of partial primary structures of the catalytic
                                                                                                                                                        P33587; O35498;
01-FBB-1994 (Rel. 28, Lact sequence update)
01-FBB-1994 (Rel. 28, Lact sequence update)
10-OCT-2003 (Rel. 42, Lact annotation update)
Vitamin-K-dependent protein C precursor (BC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                   ;
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MEDLINE-92316697; PubMed=1618739;
Tada N., Sato M., Tsujimura A., Iwase R., Hashimoto-Gotoh T.;
"Isolation and characterization of a mouse protein C cDNA.";
J. Biochem. 111:491-495(1992).
      81.2%; Score 160; DB 1; Length 461; 70.5%; Pred. No. 2.8e-19; Ive 2; Mismatches 11; Indels
                                                       1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                        461 AA
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SIMILARITY: Belongs to peptidase family SIMILARITY: Contains 2 EGF-like domains.
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  Query Match
Best Local Similarity 70.5
Matches 31, Conservative
                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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RROSITE; FOUCE2: EGF 1; 1.

RROSITE; PS01022; EGF 2; 2.

R RROSITE; PS01026; EGF 3; 1.

R ROSITE; PS01018; EGF CA; 1.

DR PROSITE; PS01011; GLU CARBOXLATION; 1.

DR PROSITE; PS01013; TRYPSIN JHS; 1.

DR PROSITE; PS01013; TRYPSIN JHS; 1.

RNO COAGHLAtion; Glycoprotein; Sexine protease;

KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation;

KW Gamma-carboxyglutamic acid; Calcium-binding; Vitamin K; Hydroxylation; Vitami
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an enail to licenseelab-sib.ch).
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PROTEIN C HEAVY CHAIN (BY SIMILARITY).
ACTIVATION PEPTIDE (BY SIMILARITY).
CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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GAWMA-CARBOXYGLUTAMIC ACID
(BY SIMILARITY).
HYDROXYLATION (BY SIMILARITY).
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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GAMMA-CARBOXYGLUTAMIC ACID
(BY SIMILMARIIY)
GAMMA-CARBOXYGLUTAMIC ACID
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SWART; SW00020; GLA; 1.

FROSITE; PS00020; AST HYDROXYL; 1.

FROSITE; PS00022; BGF 1; 1.

FROSITE; PS01186; BGF 2; 2.

FROSITE; PS00026; BGF 2; 1.

FROSITE; PS00011; BGF CA; 1.

FROSITE; PS00011; GLU CARBOXYLATION; 1.

FROSITE; PS00011; GLU CARBOXYLATION; 1.

FROSITE; PS00134; TRYPSIN HIS; 1.

FROSITE; PS00134; TRYPSIN HIS; 1.
                                                                                                                                                                  EMBL; D10445; BAA01235.1; -.
EMBL; D43745; BAA07812.1; -.
EMBL; D4375; BAA07812.1; -.
ETR; JX0210; JX0210.

BTR; JX0210; JT021.

MESP; P0470; JT02.

MGD; MGI: 97771; Proc.

InterPro; IPR009003; Cys Ser trypsin.

InterPro; IPR001801; EGF Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006209; EGF_like.
InterPro; IPR002839; GIA_blood.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR000294; VitK_dep_GIA.
Pfam; PR00089; EGF; 2.
Pfam; PR00089; ISPS; 2.
Pfam; PR00729; CHYMOTRYPSIN.
PRINTS; PR00721; CHYMOTRYPSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBDUIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is frongly promited by thrombomodulin.

TISSUE SPECIFICITY: Plasma, synthesized in the liver. FTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified profein to bind calcium.

MISCELLANEOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
BY SIMILARITY.
NYERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN REF. 2).
MISSING (IN REF. 2).
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprochrombin IIA) (Anticoagulant protein C) (Blood coagulation factor XIV).
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                                                                                                                                                                                                                                                                                                         Score 140; DB 1; Length 461;
Pred. No. 7e-16;
7; Mismatches 11; Indels
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53FAAOD85B194D6E CRC64;
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-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                         51945 MW;
                                                                                                                                                                                                                                                                                                         71.1%;
59.1%;
                                                                                                                                                                                                                                                                                                                                             26; Conservative
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     Similarity
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MRRADES, 201,218, ASK hydroxyl_S.

BR INTECPE: IPR001051; Ask hydroxyl_S.

BR INTECPE: IPR001051; Ask hydroxyl_S.

BR INTECPE: IPR0010581; Gys_Ser_trypsin.

BR INTECPE: IPR0012981; GLA_blood.

BR INTECPE: IPR001294; GlA_blood.

BR INTECPE: IPR001294; Vitk_dep_GlA.

BR INTECPE: IPR001294; Vitk_dep_GlA.

BR INTECPE: IPR001294; Vitk_dep_GlA.

BR PR00129; ECF 2.

BR PR00129; ECF 2.

BR PRNTS; PR000129; ECF CA; I.

BRART; SM00109; ECF CA; I.

BRART; SM00109; ECF CA; I.

BRART; SM00109; ECF CA; I.

BRART; SM000069; ECF 2.

BROSITE; PS00101; ASX HYDROXYL; I.

BROSITE; PS01087; ECF 2.

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PROTEIN C HEAVY CHAIN (BY SIMILARITY).
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or send an email to license@isb-sib.ch).
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EGF-LIKE 2.
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PIR; S18994; S18994.
HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
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Shen L., He X., Dahlback B.;
Submitted (FEB-1956) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Wa and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DEC-1998 (Rel. 42, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprochrombin IIA) (Anticoagulant protein C) (Blood coagulation
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Pred. No. 1e-15;
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InterPro; IPR001254; Peptidase_Sl.

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InterPro; IPR001294; VitK_dep_Gla.

InterPro; IPR001294; VitK_dep_Gla.

IPR001294; VitK_dep_Gla.

IPR001294; VitK_dep_Gla.

IPR001295; CHMOTRYPSIN.

IPRNITS; PR001205; CHMOTRYPSIN.

IPRNITS; PR001205; CHMOTRYPSIN.

IPRNITS; PR001205; CHMOTRYPSIN.

IPRNITS; PR001205; CHMOTRYPSIN.

IPROSITE; PS00101; ASX HYDROXYL; 1.

IPROSITE; PS00101; ASX HYDROXYL; 1.

IPROSITE; PS010186; EGF_3; 1.

IPROSITE; PS010187; EGF_2; 2.

IPROSITE; PS010187; EGF_2; 1.

IPROSITE; PS010134; TRYPSIN HIS; 1.

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VITAMIN K-DEPENDENT PROTEIN C.

PROTEIN C LIGHT CHAIN (BY SIMILARITY).

PROTEIN C HEAVY CHAIN (BY SIMILARITY).

ACTIVATION PEPTIDE (BY SIMILARITY).

CLEAVAGE (BY THROMBIN) (BY SIMILARITY).
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GAMMA-CARBOXYGLUTAMIC ACID
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EGF-LIKE 2
IPR009003, Cys_Ser_trypsin.
IPR001801, EGF_Ca.
IPR006209, EGF_like.
IPR005383, GLA_blood.
IPR006210, IEGF.
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Matches

8

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DR InterPro; IPR001881; EGF Ca.

InterPro; IPR002209; EGF_like.

DR InterPro; IPR002209; EGF_like.

DR InterPro; IPR002210; IEGF

InterPro; IPR0012154; Peptidase_S1.

DR InterPro; IPR0012154; Peptidase_S1.

InterPro; IPR001214; VitK_dep_GlA.

DR Ffam; PP00008; EGF; 2.

PFam; PP000009; EGF; 2.

DR PRINTS; PR00101; GLABLOOD.

DR PRINTS; PR00101; GLABLOOD.

DR PRINTS; PR00101; GLABLOOD.

DR SWART; SW00006; EGF; 2.

SWART; SW00006; EGF; 2.

DR PROSITE; PS00101; ASX_HYDROXYL; 1.

PROSITE; PS01018; EGF_2; 2.

DR PROSITE; PS01018; EGF_2; 2.

PROSITE; PS01018; EGF_2; 2.

DR PROSITE; PS01018; EGF_2; 3.

PROSITE; PS01013; TRYPSIN_HIS; 1.

PROSITE; PS01014; GlU CARGOXTCHIN; Scrinc protease; Signal.

Blood coagulation; Glycoprotein; Scrinc binding; Vitemin K; Hydroxylation; Glycopropen 1.

ST SIGNAL 1.

ST SIGNAL 1.

DR PROSITE; PS01014; TRYPSIN_ER; 1.

DR PROSITE; PS01014; TRYPSIN_ER; 1.

PROSITE; PS01014; TRYPSIN_E
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CLEAVAGE (BY THROMBIN) (BY
SIMILARITY).
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CHARGE RELAY SYSTEM.
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CHARGE RELAY SYSTEM.
BY SIMILARITY.
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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GAMMA-CARBOXYGLUTAMIC ACID (BY
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VITAMIN K-DEPENDENT PROTEIN
PROTEIN C LIGHT CHAIN (BY
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GAMMA-CARBOXYGLUTAMIC ACID
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PROTEIN C HEAVY CHAIN (BY
SIMILARITY).
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EGF-LIKE 2.
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         thrombomodulin complex.

-1 SIMILARITY: Belongs to peptidaee family S1.

-1 SIMILARITY: Contains 2 EGF-like domains.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!-SUBUNIT: Synthesized as a single chain precursor, which is cleaved into a light chain and a heavy chain held together by a disulfide bond. The enzyme is then activated by thrombin, which cleaves a tetradecapeptide from the amino end of the heavy chain; this reaction, which occurs at the surface of endothelial cells, is strongly promoted by thrombomodulin.
-!- FIRSUE SPECIFICITY: Plasma: Synthesized in the liver.
-!- FTM: The vitamin K-dependent, enzymatic carboxylation of some Glu residues allows the modified protein to bind calcium.
-!- MISCELLANBOUS: Calcium also binds, with stronger affinity to another site, beyond the GLA domain. This GLA-independent binding site is necessary for the recognition of the thrombin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Porcine factor V: cDNA cloning, gene mapping, three-dimensional protein modeling of membrane binding sites and comparative anatomy of domains.";
Cell. Mol. Life Sci. 58:148-159(2001).
-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids.
-!- CATALYTIC ACTIVITY: Degradation of blood coagulation factors Va and VIIIa and VIIIa.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Liver;
MEDLINE-21121490; PubMed=11229814;
Gzinm D.R., Colter M.B., Braunschweig M., Alexander L.J., Neame P.J.,
Kim H.K.W.;
                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vitamin-K-dependent protein C precursor (EC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI TaxID=9923;
133 133 N-LINKED (GLCNAC. .) (POTENTIAL)
287 287 N-LINKED (GLCNAC. .) (POTENTIAL)
352 352 N-LINKED (GLCNAC. .) (POTENTIAL)
458 AA, 51087 MW, D75A5F990C8F29D7 CRC64;
                                                                                                                                                             ..
0
                                                                                                          70.1%; Score 138; DB 1; Length 458; 59.1%; Pred. No. 1.5e-15; ative 4; Mismatches 14; Indels
                                                                                                                                                                                                                      1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                                                                                                                                                        459 AA
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InterPro; IPR009003; Cys_Ser_trypsin.
                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
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HSSP; P04070; 1PCU.
MEROPS; S01.218; -.
                                                                                                                               Local Similarity 59.1
les 26; Conservative
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                  CARBOHYD
CARBOHYD
SEQUENCE
  CARBOHYD
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MEDLINE-83213514; PubMed=6406503;
Johnson A.E., Esmon N.L., Laue T.M., Esmon C.T.;

Structural changes required for activation of protein C are induced by Ca2+ binding to a high affinity site that does not contain gamma-carboxyglutamid acid.";

J. Biol. Chem. 258:554-550(1983):

-!- FUNCTION: Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa
                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=8614826; PubMed=6091100;
MEDLINE=8614826; PubMed=6091100;
MCG111ivray R.T.A.;
"Cloning and sequencing of liver cDNA coding for bovine protein C.";
Proc. Natl. Acad. Sci. U.S.A. 81:5653-5656(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 197-456, AND CARBOHYDRATE-LINKAGE SITES ASN-289; ASN-350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE=83213513; PubMed=6304092;
BSmon N.L., Debault L.E., Bsmon C.T.;
"Proteolytic formation and properties of gamma-carboxyglutamic acid-
                                                                                                                                                                                                                                                                                                                                                                                Vitamin-K-dependent protein C precursor (BC 3.4.21.69)
(Autoprothrombin IIA) (Anticoagulant protein C) (Blood coagulation
factor XIV) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Sukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
                (GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
(GLCNAC. . .) (POTENTIAL)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=83169769; PubMed=6572939; Drakenberg T., Fernlund P., Roepstorff P., Stenflo J.; Bera-hydroxyasparric acid in vitamin K-dependent protein C."; Proc. Natl. Acad. Sci. U.S.A., 80:1802-1806(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stenflo J., Ferniund P., "Amino acid sequence of the heavy chain of bovine protein C. J. Biol. Chem. 257:12180-12190(1982).
                                                                                                         DB 1; Length 459;
                                                                                                                                          14; Indels
                                                                                                                                                                     1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                           424 BY SIMILARITY.
138 N-LINKED (GLCNAC. . .) (PO
292 N-LINKED (GLCNAC. . .) (PO
353 N-LINKED (GLCNAC. . .) (PO
51866 MW, 8541AAC14CC16D09 CRC64;
                                                                                                    62.4%; Score 123; DB 1;
52.3%; Pred. No. 5.4e-13;
iive 7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                         21-JTL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                456 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domainless protein C.";
J. Biol. Chem. 258:5548-5553(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND ASN-366.
MEDLINE=83007326; PubMed=6896877;
                                                                                                                    1 Similarity 52.3
23; Conservative
                                                                                                                                                                                                                                                                                              STANDARD;
396
138
292
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459 AA;
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P00745;
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CARBOHYD
SEQUENCE
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Matches
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CC -- CALATIC ACTUATIVE, Degradation of blood coagulation factors was an analyzabolizids.

CC -- CALATIC ACTUATIVE, Degradation of blood coagulation factors was compared by a failtiffee bood degradation which concerns at the autice of another base, chain this a recently which concerns a the autice of another late.

CC -- Figure Springing the manner of the heavy Chain this a restrict which concerns a the autice of another late.

Fractionally promoted by thrombondalin.

-- Figure Springing the manner of the heavy Chain this are another late and the autice of another late.

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Matches

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STRUCTURE BY NMR OF 85-126.
MEDLINE-91084483; PubMed=2261466;
Selander M., Persson E., Stenflo J., Drakenberg T.;
"IH NMR assignment and secondary structure of the Ca2(+)-free form of the amino-terminal epidermal growth factor like domain in coagulation
                                                                         SEQUENCE OF 183-492, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
MEDLINE=76053069; PubMed=1059093;
Titani K., Fujikawa K., Enfield D.L., Ericsson L.H., Walsh K.A.,
Neurath H.;
                                                                                                                                                                                         SEQUENCE OF 183-233, AND CARBOHYDRATE-LINKAGE SITES.
MEDLINE=94062825, PubMed=8243461;
Indow K., Morita T.;
"Identification of O-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate Eur. J. Biochem. 218:153-163(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujikawa K., Titani K., Davie E.W.;
"Activation of bovime factor X (Stuart factor): conversion of factor Xa-alpha to factor Xa-bers.",
Proc. Natl. Acad. Sci. U.S.A. 72:3359-3363(1975).
                                                                                                                                                                                                                                                                                                                                                                                                Neurath H., Davie E.W.;
Boyine factor X. ia (activated Stuart factor). Evidence of homology with mammalian serine proceases.";
Biochemistry 11:4899-4903(1972).
                                                                                                                                                                                                                                                                                                                                            ACTIVE SITE.
MEDLINE=73053314; PubMed=4264286;
Titani K., Hermodson M.A., Fujikawa K., Ericsson L.H., Walsh K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-84185716; PubMed-6546930; Sugo T., Bjoerk I., Holmgren A., Stenflo J.; Calcium-binding properties of bovine factor X lacking the gamma-carboxyglutamic acid-containing region."; J. Biol. Chem. 259:5705-5710(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDINE-5240652; PubMed=1527084; Selander-Sunnerhagen M., Ullner M., Persson E., Teleman O., Stenflo J., Drakenberg T.; "How an epidermal growth factor (EGF)-like domain binds calcium: resolution NMR structure of the calcium form of the NH2-terminal
                                                                                                                                            Bovine factor X1 (Stuart factor): amino-acid sequence of heavey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=86140210; PubMed=3949800;
Morita T., Jackson C.M.;
"Localization of the structural difference between bovine blood coagulation factors XI and X2 to tyrosine 18 in the activation peptide.";
J. Biol. Chem. 261:4008-4014(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Three-dimensional structure of the apo form of the N-terminal BGF-like module of blood coagulation factor X as determined by appettroscopy and simulated folding."; Blochemistry 31:5974-5983(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92329412; PubMed=1627540;
Ullner M., Selander M., Persson E., Stenflo J., Drakenberg T.,
        "The occurrence of beta-hydroxyaspartic acid in the vitamin K-dependent blood coagulation zymogens."; Biochem. Biophys. Res. Commun. 115:8-14(1983).
                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 72:3082-3086(1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=76053121; PubMed=1059122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 29:8111-8118(1990).
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                                                                                                                                                            chain.'
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Fung M.R., Campbell R.M., McGillivray R.T.A.;
Blood coagulation factor X mRNA encodes a single polypeptide chain
containing a prepro leader sequence.";
Nucleic Acids Res. 12:4481-4492 (1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of the light chain of bovine factor X1 (Stuart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
MCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 41-180.
MEDLINE-80130563; PubMed=6766735;
Enfield D.L., Ericsson L.H., Fujikawa K., Walsh K.A., Neurath H.,
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13-AUG-1987 (Rel. 05, Last sequence update)
LP-MAR-2004 (Rel. 43, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.9%; Score 122; DB 1; Length 456; 50.0%; Pred. No. 7.9e-13; Live 9; Mismatches 12; Indels
GAMMA-CARBOXYGLUTAMIC ACID.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAF6833F894C209 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .).
(GLCNAC. . .).
(GLCNAC. . .).
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MEDLINE-83308813; PubMed=6688526;
MCMullen B.A., Fujikawa K., Kisiel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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les 21; Conservative
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     Bos taurus (Bovine).
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   FA10 BOVIN
P00743;
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                                                                                                                                                          MEDLINE=96387194; PubMed=8794734;
Sunnerhagen M., Olah G.A., Stenflo J., Forsen S., Drakenberg T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | PSULLED BGF_3; | PSULLED BGF_3; | PSO1187; EGF_3; | PSO1187; EGF_CA; | PSO1187; EGF_CA; | PSO1240; TRYPSIN DOM; | PSO0134; TRYPSIN HIS; | PSO0135; TRYPSIN BS; PSO0135; TRYPSIN BS; | PSO0135; TRYPSIN BS; | PSO0135; | PSULLED BS; | PSULLED 
like domain in coagulation factor X.";
J. Biol. Chem. 267:19642-19649(1992).
[13]
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SMART; SMO0069; GLA; 1.
SMART; SMO0020; Tryp SPc; 1.
PROSITE; PS00010; ASX HYDROXIL; 1.
PROSITE; PS01186; EGF 1; 1.
PROSITE; PS01186; EGF 2; 2.
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                                                                     STRUCTURE BY NMR OF 41-126
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PDB; 1CCF; 31-MAY-94.
PDB; 1WHE; 15-MAY-97.
PDB; 1WHF; 15-MAY-97.
PDB; 1IOD; 21-JAN-03.
PDB; 1KIG; 28-OCT-98.
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GlycoSuiteDB; P00743;
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Glycoprotein, Hydrolase, Serine protease, Plasma, Blood coagulation, Gamma-carboxyglutamic acid, Hydroxylation, Calcium-binding, Vitamin K, Signal, Zymogen, EGF-like domain, Repeat, Sulfation, 3D-structure.
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EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Messier T.L., Pittman D.D., Long G.L., Kaufman R.J., Church W.R.; "Cloning and expression in COS-1 cells of a full-length cDNA encoding thuman cosquiation factor X."; Gene 99:291-294 (1991).
                                                                                                                                                                             ACTIVATED FACTOR XA, HEAVY CHAIN.
MAY BE REMOVED BUT IS NOT NECESSARY FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=87026600; PubMed=3768336;
Leytus S.P., Foster D.C., Kurachi K., Davie E.W.;
Gene for human factor X: a blood coagulation factor whose gene organization is essentially identical with that of factor IX and protein C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Riedar M.J., Carrington D.P., Chung M.-W., Lee K.L., Ozuma M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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P00742; Q14340;
21-JUL-1986 [Rel. 01, Created)
01-OCT-1989 [Rel. 12, Last sequence update)
10-OCT-2003 [Rel. 42, Last annotation update)
Coagulation factor X precursor [RC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 114; DB 1; Length 492;
Pred. No. 2e-11;
8; Mismatches 16; Indels
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
GAMMA-CARBOXYGLUTAMIC ACID.
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FACTOR X HEAVY CHAIN.
ACTIVATION PEPTIDE.
                                                                     POTENTIAL.
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MEDLINE=91216473; Pubmed=1902434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
                                                                   Local Similarity
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKennan K.J., Mallek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Hakesley J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
Invent A. Rodrigues S.I. N. R. Schenerch S. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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MEDLINE-94062825; PubMed-8243461;
Inoue K., Morita T.;
Inoue K., Morita T.;
Identification of 0-linked oligosaccharide chains in the activation peptides of blood coagulation factor X. The role of the carbohydrate moleties in the activation of factor X.";
Els. J. Blochem. 218:153-163(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE=86221713; PubMed=3011603;
Kaul R.K., Hildebrand B., Roberts S., Jagadeeswaran P.;
"Isolation and characterization of human blood-coagulation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5]
SEQUENCE OF 13-488 FROM N.A.
MEDLINE=85216545; PubMed=2582420;
Fung M.R., Hay C.W., McGillivray R.T.A.;
Fung M.R., Hay C.W. andinivray R.T.A.;
Fung docarriation of an almost full-length cDNA coding for human blood coagulation factor X.";
Proc. Natl. Acad. Sci. U.S.A. 82:3591-3595(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 86-179 AND 235-278. MEDLINE=93360277; PubMed=8355279; Padmanabhan K.P., Tulinsky A., Park C.H., Bode Huber K., Blankenship D.T., Cardin A.D., Kisiel W.; "Structure of human des(1-45) factor Xa at 2.2-A resolution."; J. Mol. Biol. 232:947-966(1993).
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X-ZAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 86-179 AND 235-278.
MEDLINE-98283982; PubMed=9618463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 115-488 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 22:2875-2884(1983).
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                                                                                                                                                                Lander E.S.;
"Characterization of single-nucleotide polymorphisms in coding regions
                                                                                              MEDLINE=99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Zlaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Kamata K., Kawamoto H., Honma T., Iwama T., Kim S.H.;
"Structural basis for chemical inhibition of human blood coagulation
factor Xa.";
                                                                                                                                                                                                                                                                                                                                Nat. Genet. 23:373-373 (1999).

-!- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

-!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-!-Thr and then Arg-!-Ile bonds in prothrombin to form thrombin.

-!- SUBUNIT: The two chains are formed from a single-chain precursor by the excision of two Arg residues and are held together by 1 on more disulfide bonds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glutamate residues allows the modified protein to bind calcium.
--- PTM: N- and O-Glycosylated.
--- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY PACTOR IXA (IN THE INTRINSIC PATHWAY).
--- SIMILARITY: Belongs to peptidase family $1.
--- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L. Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1-1 TISSUE SPECIFICITY: Plasma; synthesized in the liver.
-1- PIM: The vitamin K-dependent, enzymatic carboxylation of some glutamate residues allows the modified protein to bind calcium.
                                                 Proc. Natl. Acad. Sci. U.S.A. 95:6630-6635(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L29433; AAA52764.1; -.
L00390; AAA52764.1; JOINED.
L00391; AAA52764.1; JOINED.
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L00393; AAAS2764.1; JOINED.
L00394; AAAS2764.1; JOINED.
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AAA52764.1; JOINED.
AAA51984.1; -.
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EMBL; AF503510; AAM19347.1; -.
EMBL; BC046125; AAH46125.1; -.
                                                                                                                                                                                                                   Genet. 22:231-238(1999).
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                                                                                VARIANTS ILE-7 AND HIS-30.
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M33297; AAA52636.1;
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29-OCT-97
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                                                                                                                                                                                                   of human genes.
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PIR; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Spinal cord;
MEDLINE=21117044; PubMed=11171957;
Kulman J.D., Harris J.D., Xie L., Davie B.W.;
Kulman J.D., Harris J.D., Xie L., Davie B.W.;
Identification of two novel transmembrane gamma-carboxyglutamic acid proteins expressed broadly in fetal and adult tissues.";
Proc. Natl. Acad. Sci. U.S.A. 98:1370-1375(2001).
-! SUBCELLULAR LOCATION: Type I membrane protein.
-! TISSUE SPECIFICITY: Expressed in brain, lung, kidney and heart.
-! PIM: Gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin K-dependent gamma-
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TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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28-FEB-2003 (Rel. 41, Last Sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Transmembrane gamma-carboxyglutamic acid protein 3 precursor
                                                                                                                                                                                                                                              GO; GO:0005576; C:extracellular; TAS.
GO; GO:0003804; F:blood coagulation factor X activity, TAS.
GO; GO:0007596; P:blood coagulation; TAS.
                                                                                                                                                                                                                                                                                                                                      Length 488;
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DR GO; GO: 6016021; C: integral to membrane; NAS.

InterPro; IPR002383; GLA blood.

R InterPro; IPR00294; Vitk_dep_GLA.

R PEINTS; PR00001; GLABLOOD.

R SMART; SW00069; GLA; 1.

PROSITE; PS00011; GLU_CARBOXXLATION; 1.

R PROSITE; PS00011; GLU_CARBOXXLATION; 1.

PROSITE; PS00111; GLU_CARBOXXLATION; 1.

PROPEP
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CASIMON CASIMON
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55.8%; Score 110; DB 1;

Best Local Similarity 43.2%; Pred. No. 9.3e-11;

Matches 19; Conservative 9; Mismatches 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA
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                                                                                                                                                            MEROPS; S01.216; -.
GlycoSuiteDB; P00742;
                                                                                                                                                                                        Genew; HGNC:3528; F10.
                                                                                                                                   25-FEB-03.
                                                         28-JAN-03.
25-FEB-03.
25-FEB-03.
                                                                                                                   25-FEB-03
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                                                         1MO6;
1NFU;
1NFW;
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                                    LM05;
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PDB; 1KS;
PDB; 1KY;
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- I- FUNCTION: Factor Xa is a vitamin K-dependent glycoprotein that converts prothrombin to thrombin in the presence of factor Va, calcium and phospholipid during blood clotting.

- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Thr and then Arg-|-11e bonds in prothrombin to form thrombin.

- SUBUNIT: The two chains are formed from a single-chain precursor more disulfide bonds.

- The FIM: The vitamin K-dependent, enzymatic carboxylation of some continues allows the modified protein to bind calcium (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: N- and O-glycosylated (By similarity).
-!- PTM: THE ACTIVATION PEPTIDE IS CLEAVED BY FACTOR IXA (IN THE INTERNSIC PATHWAY), OR BY FACTOR VIIA (IN THE EXTRINSIC PATHWAY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
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15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor X precursor (EC 3.4.21.6) (Stuart factor).
                                                                                                                                                                                                                     similarity 54.3%; Score 107; DB 1; Length 231; Similarity 43.9%; Pred. No. 1.3=10; Conservative 8; Mismacches 15; Indels 8; Conservative 15; Indels
                                                                                                                                                                                                                                                                                      8; Mismatches 15; Indels
      EXTRACELLULAR (POTENTIAL).
                    20 78 EXTEACELLULAR (POTENTIAL)
79 101 POTENTIAL
102 231 CYTOPLASMIC (POTENTIAL).
23 60 GLA.RICH.
231 AA; 25848 MW; 8A373E4848490D81 CRC64;
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PROTEIN 3
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BGF 2.
BGF Ca.
BGF Ca.
BGF Ike.
GGA blood.
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InterPro; IPR000152; Asx_hydroxyl InterPro; IPR009003; Cys_Ser_tryps InterPro; IPR00742; EGF_2.
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Interpro; IPR006209;
Interpro; IPR002383;
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LITERPRO) IPRO01254; Peptidase S1.

DR INTERPRO; IRRO01314; Peptidase S1A.

DR INTERPRO; IRRO00294; VitK_dep_GLA.

DR PÉRAN; PPO00069; EFF; 2.

DR PERINTS; PRO01029; CHYMOTYPEIN.

DR PRINTS; PRO01010; EGPBLOOD.

DR STRINTS; PRO01010; EGPBLOOD.

DR SWART; SM00069; GLA; 1.

DR SWART; SM00010; ASX_HYROXL; 1.

DR SWART; SM00110; ASX_HYROXL; 1.

DR PROSITE; PS00110; ASX_HYROXL; 1.

DR PROSITE; PS00110; ASX_HYROXL; 1.

DR PROSITE; PS001187; EGF_CA; 1.

DR PROSITE; PS001187; TRYPSIN DOW; 1.

DR PROSITE; PS001187; TRYPSIN D
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FACTOR X LIGHT CHAIN.
FACTOR X LIGHT CHAIN.
ACTIVATION PEPTIDE.
ACTIVATED FACTOR XA, HEAVY CHAIN.
EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
SEFLIKE 2.
SERINE PROTEASE.
GAMMA-CARROXYGIUTAMIC ACID (BY
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CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
BY SIMILARITY.
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TISSUB-Liver;

RETISTON TO 395.

TISSUB-Liver;

Ruiz S.R., Blajchman M.A., Clarke B.J.;

Converted to factor VIIa by factor XII, factor IXI, or thrombin by minor proteolysis. In the presence of tissue factor X to factor X to factor IXI, or thrombin by minor proteolysis. In the presence of tissue factor X to factor X to factor IXI in the presence of tissue factor X to factor IX to similarity).

Converted to factor VIIa then converts factor X to factor X in the presence of tissue factor X to factor IX to factor IXI in the presence of tissue factor and calcium (By similarity).

Converted to factor IXI in the presence of tissue factor in factor X to factor X in the presence of tissue factor in the presence of tissue factor in factor X in factor X in the presence of tissue factor in factor X in the presence of tissue factor in factor X in the presence of tissue factor in factor X in the presence of tissue factor in factor X in the presence of tissue factor IXI in factor X in the presence of tissue factor in factor X in the presence of tissue factor in the presence of tissue factor IXI in the terodimer of a light chain and a heavy chain linked by IXI is the vitamin K-dependent, enzymatic carboxylation of some of putch and the modified protein to bind calcium (By cimilarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brothers A.B., Clarke B.J., Sheffield W.P., Blajchman M.A., "Complete nucleotide sequence of the cDNA encoding rabbit coagulation
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                        FA7 RABIT STANDARD; PRT; 444 AA.
P98139; P79224;
01-FEB-1996 (Rel. 33, Created)
10-GT-2003 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
  N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
3A39FA85AF2A6D11 CRC64;
                                                                                                                                                   ö
                                                                                                  Length 490;
                                                                                                                                                 16; Indels
                                                                                                                                                                                             1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                                         41 ANSFLEELKKGNLERECMEENCSYEEALEVFEDREKTNEFWNKY 84
                                                                                             Query Match 52.3%; Score 103; DB 1; Best Local Similarity 43.2%; Pred. No. 1.4e-09; Matches 19; Conservative 9; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity).
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; S01.215; -.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR009003; Cyg_Ser_trypsin.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thromb. Res. Suppl. 69:231-238(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93190306; PubMed=8383365;
187 187 N
205 205 N
490 AA; 53965 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U77477; AAB37326.1; -.
HSSP; P08709; 1FAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor VII.";
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41

1 ANSFLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFW

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GLA-RICH VIT HEAVY CHAIN.

GLA-RICH CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).

EGF-LIKE 2.

SERINE PROTEASE.

CLEAVAGE (BY FACTOR XA, FACTOR XIIA, FACTOR IXA, OR THROMBIN) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                     PROSITE; PS01062; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00118; EGF_CA; 1.
PROSITE; PS00011; GLU_CARBOXYLATION; 1.
PROSITE; PS00013; TRYPSIN_HTS; 1.
PROSITE; PS00135; TRYPSIN_HTS; 1.
PROSITE; PS00135; TRYPSIN_ERF; 1.
PROSITE; PS00135; TRYPSIN_ERF; 1.
PROSITE; PS00136; TRYPS
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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HYDROXYLATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O481ABC4FE5427F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FACTOR VII LIGHT CHAIN. FACTOR VII HEAVY CHAIN.
              InterPro; IPR006209; EGF_like.
InterPro; IPR006209; EGF_like.
InterPro; IPR001284; PepEidase_SI.
InterPro; IPR001284; PepEidase_SI.
InterPro; IPR001284; PepEidase_SI.
InterPro; IPR000294; Vitk_dep_Gla.
Pfam; PF00008; EGF; 2.
Pfam; PF00009; Irypsin; 1.
PRINTS; PR00001; EGFBLOOD.
SWART; SW00129; EGF_CA; 1.
SWART; SW00069; GIA; 1.
PRINTS; PR00001; GLABLOOD.
SWART; SW00069; GIA; 1.
PR0SITE; PS00010; ASK HYDROXYL; 1.
PROSITE; PS00010; ASK HYDROXYL; 1.
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    IPR001438;
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Best Local Similarity
Matches 19; Conserv
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CARBOHYD
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MEDLINE=91344709; PubMed=2129367;
Iwanaga S., Nishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T.;
"A new trisaccharide sugar chain linked to a serine residue in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 61-466, AND POST-TRANSLATIONAL MODIFICATIONS.
MEDLINE=89088153; PubMed=3264725;
Thim Li. Bjoern S., Christensen M., Nicolaisen E.M., Lund-Hansen T., Pedersen A.H., Hedner U., Andrer U., Educor Mila from plasma and transfected baby hamster kidney cells.";
Bjochemistry 27:7785-7793(1988).
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Mishimura H., Kawabata S., Kisiel W., Hase S., Ikenaka T., Takao T.,
Nishimura H., Kawabata S.,
Nishimonishi Y., Iwanaga S.,
"Identification of a disaccharide (Xyl-Glc) and a trisaccharide
(Xyl2-Glc) O-glycosidically linked to a serine residue in the first
epidermal growth factor-like domain of human factors VII and IX and
protein Z and bovine protein Z.,
J., Biol. Chem. 264:20320-20325(1989).
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98709; 014339;
01-074-1988 (Rel. 06, Last sequence update)
01-074-2033 (Rel. 42, Last annotation update)
Cosquilation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator) (Eptacog alfa).
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MEDLINE=87260948; PubMed=3037537;
MEDLINE=873., Grant F.J., Haldeman B.A., Gray C.L., Insley M.Y.,
Hagen F.S., Murray M.J.;
Hagen F.S., Murray M.J.;
"Nucleotide sequence of the gene coding for human factor VII, a
vitamin K-dependent protein participating in blood coagulation.";
Proc. Natl. Acad. Sci. U.S.A. 84:5158-5162(1987).
                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYDRATE-LINKAGE SITES SER-112 AND SER-120.
MEDLINE=91250411; PubMed=1904059;

MEDLINE=91250411; PubMed=1904059;

Bjoern S., Poster D.C., Thim L., Wiberg F.C., Christensen M., Komiyama Y., Pedersen A.H., Kisjel W.;

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MEDLINE-86205965; PubMed=1486420;
MEDLINE-86205965; Cl., O'Hara P.J., Grant F.J., Saari G.C.,
Hagen F.S., Gray C.L., O'Hara P.J., Kislel W., Kurachi K.
Woodbury R.G., Hart C.E., Insley M.Y., Kislel W., Kurachi K.
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Proc. Natl. Acad. Sci. U.S.A. 83:2412-2416(1986).
                     80
40 ANSFLEELRPGSLERECKEELCSFEEAREVFOSTERTKOFW
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                               RESULT 12
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Gaps

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Conservative

factor RESULT 13 TMG1_HUMAN ઠે g first EGF-like domain of clotting factors VII and IX and protein Z.", Adv. Exp. Med. Biol. 281:121-131(1990). MEDLINE=92340074; PubMed=1634227;
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polymorphism in the factor VII gene (F7).";
Hum. Genet. 89:497-502(1992). VARIANT VAL-354.
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MEDILTE=95072589; PubMed=7981691;
MEDILTE=95072589; PubMed=7981691;
Rodeghiero F., Marchtetti G.;
"Topologically equivalent mutations causing dysfunctional coagulation MEDLINE=99126538; PubMed=9925787; Zhang E., St Charles R., Tulinsky A.; "Structure of extracellular tissue factor complexed with factor VIIa inhibited with a BPTI mutant."; U. Mol. Biol. 285:2089-2104(1999). MEDLINE=94264305; PubMed=8204879; Chaing S., Clarke B., Sridhara S., Chu K., Friedman P., Vandusen W., Roberts H.R., Blajchman M., Monroe D.M., High K.A.; Severe factor VII deficiency caused by mutations abolishing the Cleavage site for activation and altering binding to tissue factor."; Blood 83:3524-3535(1994). O'Brien D.P., Gale K.M., Anderson J.S., McVey J.H., Miller G.J., Meade T.W., Tuddenham E.G.D.; "Purification and characterization of factor VII 304-Gln: a variant molecule with reduced activity isolated from a clinically unaffected ·. Ŧ "Solution structure of the N-terminal EGF-like domain from human factor VII."; Takamiya O., Kemball-Cook G., Martin D.M.A., Cooper D.N., von Felten A., Meili E., Hahn I., Prangnell D.R., Lumley H., Tuddenham E.G.D., McVey J.H.;
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(115His and 333Ser) in the human coagulation factor VII gene.";
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"Characterization of single-nucleotide polymorphisms in coding regions
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Tamary H., Fromovich Y., Shalmon L., Reich Z., Dym O., Lanir N.,
Brenner B., Paz M., Luder A.S., Blau O., Korostishevsky M.,
Zaizov R., Seligsohn U.;
"Alaz44Val is a common, probably ancient mutation causing factor VII
deficiency in Moroccan and Iranian Jews.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS ASP-295 AND GLN-413.
MEDLINE=99318093; PubMed=10391209;
Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.
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WEDLINE-97001216; PubMed-8844208;
Bernardi F., Castaman G., Pinotti M., Ferraresi P., di Iasio M.G.,
Lunghi B., Rodeghiero F., Marchetti G.;
"Mutation pattern in clinically asymptomatic coagulation factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Factor VII Morioka (FVII L-26P): a homozygous missense mutation in
the signal sequence identified in a patient with factor VII
deficiency.";
                                                                                    VARIANT MIE HIS-307.
MEDLINE-95064662; PubMed-7974346;
Ohiwa M., Hayashi T., Wada H., Minamikawa K., Shirakawa S.,
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"Factor VI Mie: homozygous asymptomatic type I deficiency caused an amino acid substitution of His (CAC) for Arg(247) (CGC) in the
                                                                                                                                                                                                                                                                                                                                                                                       VARIANT MET-419.
MEDLINE=66247510; PubMed=8652821;
MEDLINE=66247510; PubMed=8652821;
MEDLINE=56247510; PubMed=8652821;
"A Thr359Met mutation in factor VII of a patient with a hereditary deficiency causes defective secretion of the molecule.";
Blood 87:5085-5094(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98112461; PubMed-9452082;
Alahinawi C., Scerri C., Galdies R., Aquilina A., Felice A.E.;
"Two new missense mutations (P134T and A244V) in the coagulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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Ozawa T., Takikawa Y., Niiya K., Ejiri N., Suzuki K., Sato S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.3%; Score 99; DB 1; Length 466; Conservative 48.8%; Pred. No. 6.5e-09; Conservative 4; Mismarches
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factors VII (294Ala-->Val) and X (334Ser-->Pro).";
Hum. Mol. Genet. 3:1175-1177(1994).
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                                                                                                                                                                                                                                                                                                catalytic domain.";
Thromb. Haemost. 71:773-777(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Haematol. 101:47-49(1998).
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Nat. Genet. 22:231-238(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hum. Mutat. 8:108-115(1996).
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Best Local Similarity
Matches 20; Conserv
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Rattus norvegicus (Rat).
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                                                      28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-Tannamembrane gamma-carboxyglutamic acid protein 1 precursor (Proline-rich Gla protein 1) (Proline-rich gamma-carboxyglutamic acid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kulman J.D., Harris J.E., Haldeman B.A., Davie E.W.;
"Primary structure and tissue distribution of two novel proline-rich
gamma-carboxyglutamic acid proteins.";
Proc. Natl. Acad. Sci. U.S.A. 94:9058-9062(1997).
-! TISSUE SPECIFICITY: Highly expressed in the spinal cord.
-!- TISSUE SPECIFICITY: Highly expressed in the spinal cord.
-!- PTM: Gla residues are produced after subsequent posttranslational modifications of glutamate by a vitamin K-dependent gamma-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID
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                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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218 AA; 24947 MW; 26538A61AB0AEB98 CRC64;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00011, GLU CARBOXYLATION, 1.
Gamma-carboxyglutamic acid, Vitamin K, Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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GO; GO:0005887; C:integral to plasma membrane; TAS.
InterPro; IPR002383; GLA blood.
InterPro; IPR00294; VitK dep GLA.
   218 AA.
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MEDLINE=97404347; PubMed=9256434;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000294; VitK of Pfam; PF00594; gla; 1. PRINTS; PRO0001; GLABLOOD.
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STANDARD;
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                                                                                                                                                                                                                                             PRRG1 OR TMG1 OR PRGP1.
Homo sapiens (Human).
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les 17; Conserv
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IMG1 HUMAN
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P18292;
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DOMAIN
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SEQUENCE
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THRB RAT
ID THRB
AC P1829
DT 01-NO
DT 28-FE
DE Proch
GN F2
STATE THE TRANSPORT OF STREET STATES AND STREET
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01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Prothrombin precursor (EC 3.4.21.5).

01-NOV-1990 (Rel. 16, Created)

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                                                                                                                                                                                                                                                                                                                              MEDINE=92112913; PubMed=1557383;

RETINE=92112913; PubMed=1557383;

RETINE=92112913; PubMed=1557383;

RETINE=92112913; PubMed=1557383;

RETINE CARTERIAL CHARACTERIAL CHARACTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation
                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to peptidase family SI. -!- SIMILARITY: Contains 2 kringle domains.
                                                                                                                                                  STRAIN-Sprague-Dawley, TISSUE-Liver,
MEDLINE-90332456; Pubmed-2377469;
Dihanich M., Monard D.;
"cDNA sequence of rat prothrombin.";
Nucleic Acids Res. 18:4251-4251(1990).
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Incerpro, IPR00283, GlA_blood.
Interpro, IPR001254, Peptidase_S1.
Interpro, IPR001254, Peptidase_S1.
Interpro, IPR001354, Peptidase_S1A.
Interpro, IPR001366, Peptidase_S1A.
Interpro, IPR003966, Peptidase_GLA_pr.
Interpro, IPR003966, Vitk_dep_GLA.
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Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN,
PRINTS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52835; CAA37017.1; -.
EMBL; M81397; AAA42240.1; -.
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PRINTS; PRO1505; PROTHROWBIN.
ProDom; PD000395; Kringle; 2.
SWART; SM00069; GLA, 1.
                                                                                                                                                                                                                                                                                                                SEQUENCE OF 383-617 FROM N.A.
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                                                                                                                                 SEQUENCE FROM N.A.
                                                                       NCBI_TaxID=10116;
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RD SEQUENCE PROM N.A.

RATAINEFVENON TISSUE-Liver;

RA Strausberg R.D. Feingold E.A. Grouse L.H., Derge J.G.,

RA Strausberg R.D. Collins F.S. Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F. Zeeberg B. Buttow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jeden H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Altschul M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheerz T.E.,

RA Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Paley J., Hellcon E., Ketteman M., Madan A., Kodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RY Human and mouse cDNA sequences:";

RY human and mouse cDNA sequences:";

RY Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
              Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                    STRAIN=C57BL/6; TISSUB=Liver;
STRAIN=C57BL/6; TISSUB=Liver;
MEDLINE=91025551; PubMed=2222810;
Frizzner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
"Chazetterization of the cDNA coding for mouse prothrombin and localization of the gene on mouse chromosome 2.";
DNA Cell Biol. 9:487-498(1990).
                                             NCBI_TaxID=10090;
              J; Glycoprotein; Repeat;
acid; Acute phase; Liver;
                                                                                                                                                                                                                                                 SERINE PROTEASE.
CLEAVAGE (BY THROMEIN).
CLEAVAGE (BY PACTOR XA).
CLEAVAGE (BY PACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
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ACTIVATION PEPTIDE (FRAGMENT
ACTIVATION PEPTIDE (FRAGMENT
THROMBIN LIGHT CHAIN (A).
THROMBIN HEAVY CHAIN (B).
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BY SIMILARITY.
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DR PROSITE; PS00011; GLÜ CARBOXYLATION; 1.

PROSITE; PS00011; GLÜ CARBOXYLATION; 1.

DR PROSITE; PS0070; KRINGLE 1; 2.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_ER; 1.

W PROSITE; PS00134; TRYPSIN_ER; 1.

W PROSITE; PS00135; TRYPSIN_ER; 1.

W Hydrolase; Serine protease; Kringle; Signal.

I SIGNAL

CHAIN

CHAIN

44 677
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KRINGLE 2.
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DOMAIN
DOMAIN
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TRSUENCE OF 384-618 FROM N.A.

TRSUELNINES 2212913; PubMed=1557383;

MEDINE=59212913; PubMed=1557383;

RA anfield D.K., Macgillivray R.T.;

"Partial characterization of vertebrate prothrombin cDNAs:
anfifferent and sequence analysis of the B chain of thrombin from and sequence analysis of the B chain of thrombin from the different and sequence analysis of the B chain of thrombin from the different and sequence analysis of the B chain of thrombin from RT In the different and sequence from the different sequence of the Brown of Brow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation by factor Xa.
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42.2%; Pred. No. 1.2e-06;
ive 6; Mismatches 19; Indels
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Local Similarity 42.2 les 19; Conservative

Best Loc Matches

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RESULT 15 THRB_MOUSE

GETTTE

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                  KALNALE 2.
SERINE PROTEASE.
CLEAVAGE (BY THROMEIN).
CLEAVAGE (BY PACTOR XA).
CLEAVAGE (BY FACTOR XA).
CLEAVAGE (BY FACTOR XA).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
GAWMA-CARBOXYGLUTAMIC ACID.
BY SIMILARITY.
                                                                                                                                                                             MOD_RES
MOD_RES
MOD_RES
MOD_RES
DISULFID
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Gaps
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H
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43.9%; Score 86.5; DB 1; Length 618;
Best Local Similarity 42.2%; Pred. No. 1.2e-06;
Matches 19; Conservative 6; Mismatches 19; Indels
479 INTERCHAIN (BY SIMILARITY).
404 BY SIMILARITY.
547 BY SIMILARITY.
591 BY SIMILARITY.
122 N-LINKED (GLCNAC. .).
413 N-LINKED (GLCNAC. .).
553 N-LINKED (GLCNAC. .).
553 N-LINKED (GLCNAC. .).
                                                                                                                                                                                          1 ANS-FLXXLRQGSLXRXCIXXICDFXXAKXIFEDVDDTLAFWSKH 44
                                                                                                                                                                                                            44 ANSGFLEELRKGNLERECVEEQCSYEEAFEALESPQDTDVFWAKY 88
                                                                                                                                                                                                                                                           Search completed: March 1, 2004, 10:03:23 Job time: 10.5 secs
  333
388
561
122
142
414
414
655
618 AA,
             DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
    DISULFID
    8
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